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NCBI

results of BLAST

BLASTP 2.2.9 [May-01-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.

RID: 1087857020-23039-205662433234.BLASTQ4

Query=

(770 letters)

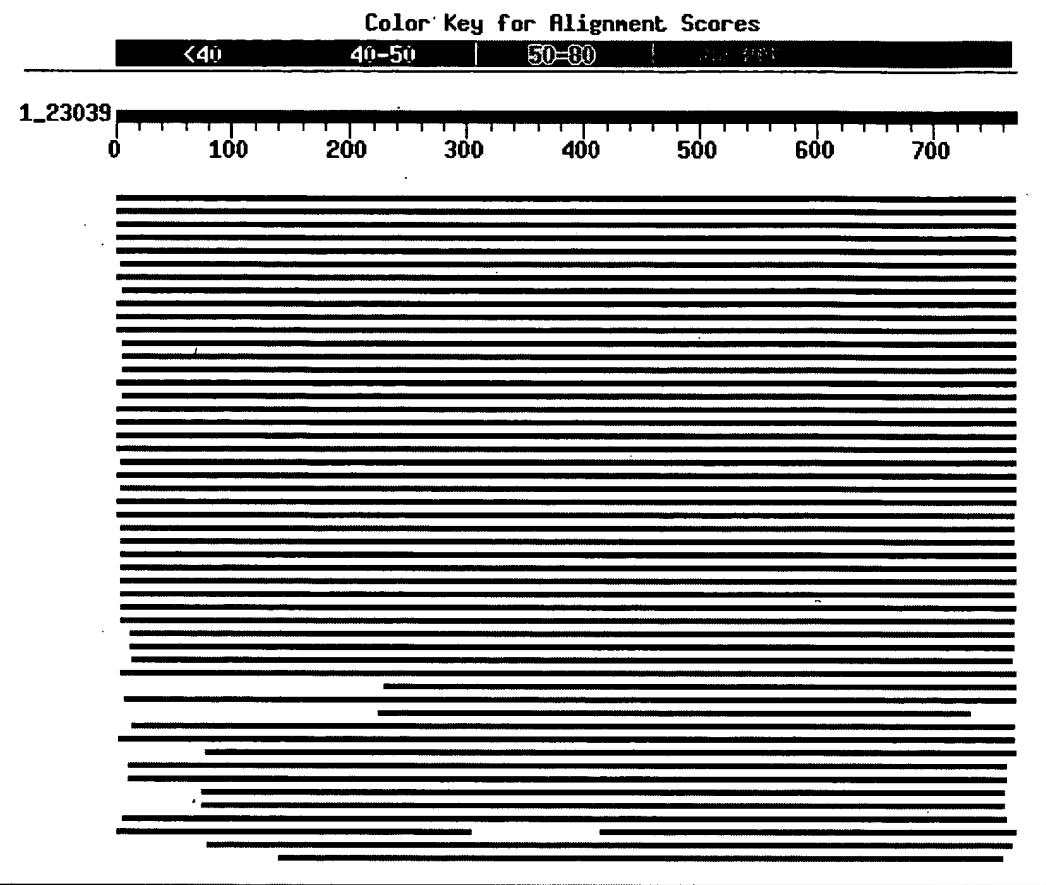
Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF excluding environmental samples
1,865,463 sequences; 619,299,334 total letters

If you have any problems or questions with the results of this search
please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Score E

Sequences producing significant alignments: (bits) Value

<u>gi 15982958 gb AAL11507.1 </u>	vacuolar H+-pyrophosphatase [Pru...]	<u>1120</u>	0.0
<u>gi 3298474 dbj BAA31523.1 </u>	ovp1 [Oryza sativa]	<u>1167</u>	0.0
<u>gi 2129950 pir S61423 </u>	inorganic diphosphatase (EC 3.6.1.1)...	<u>1194</u>	0.0
<u>gi 15982956 gb AAL11506.1 </u>	vacuolar H+-pyrophosphatase [Pru...]	<u>1186</u>	0.0
<u>gi 38488588 dbj BAD02276.1 </u>	vacuolar proton pyrophosphatase...	<u>1144</u>	0.0
<u>gi 322841 pir JC1466 </u>	inorganic diphosphatase (EC 3.6.1.1) ...	<u>1154</u>	0.0
<u>gi 3608171 dbj BAA33149.1 </u>	proton-translocating inorganic p...	<u>1182</u>	0.0
<u>gi 7436046 pir T14563 </u>	inorganic diphosphatase (EC 3.6.1.1)...	<u>1202</u>	0.0
<u>gi 2129948 pir S61424 </u>	inorganic diphosphatase (EC 3.6.1.1)...	<u>1172</u>	0.0
<u>gi 1103712 emb CAA58700.1 </u>	inorganic pyrophosphatase [Nicot...	<u>1180</u>	0.0
<u>gi 7436041 pir S72526 </u>	inorganic diphosphatase (EC 3.6.1.1)...	<u>1169</u>	0.0

gi|31580801|gb|AAP55210.1| vacuolar proton-inorganic pyroph... 1132 0.0
gi|7739779|gb|AAF69010.1| H+-pyrophosphatase [Vitis vinifera] 1109 0.0
gi|7436042|pir||S72527| inorganic diphosphatase (EC 3.6.1.1)... 1146 0.0
gi|30027157|gb|AAP06752.1| vacuolar proton-inorganic pyroph... 1166 0.0
gi|18086404|gb|AAL57660.1| At1g15690/F7H2_3 [Arabidopsis th... 1315 0.0
gi|542059|pir||S42893| inorganic diphosphatase (EC 3.6.1.1) ... 1197 0.0
gi|25901033|dbj|BAC41250.1| vacuolar proton-inorganic pyrop... 1188 0.0
gi|22532391|gb|AAM97920.1| vacuolar proton-pumping PPase [C... 1179 0.0
gi|7436047|pir||T14564| inorganic diphosphatase (EC 3.6.1.1)... 1168 0.0
gi|11527561|dbj|BAB18681.1| vacuolar proton-inorganic pyrop... 1157 0.0
gi|3402487|dbj|BAA32210.1| Vacuolar proton pyrophosphatase ... 1311 0.0
gi|45479863|gb|AAS66771.1| PPase [Hevea brasiliensis] 1207 0.0
gi|2827755|sp|P21616|AVP3_PHAAU| Pyrophosphate-energized vac... 1171 0.0
gi|41023649|emb|CAF18416.1| proton translocating pyrophosph... 1140 0.0
gi|38045977|gb|AAR08913.1| pyrophosphate-energized vacuolar... 1279 0.0
gi|38488590|dbj|BAD02277.1| vacuolar proton pyrophosphatase... 1175 0.0
gi|2129949|pir||S61422| inorganic diphosphatase (EC 3.6.1.1)... 1190 0.0
gi|18274925|sp|Q06572|AVP3_HORVU| Pyrophosphate-energized va... 1153 0.0
gi|7436043|pir||T07801| probable inorganic diphosphatase (EC... 1178 0.0
gi|15218279|ref|NP_173021.1| pyrophosphate-energized vacuol... 1316 0.0
gi|1076627|pir||S54172| inorganic diphosphatase (EC 3.6.1.1)... 1203 0.0
gi|19310433|gb|AAL84953.1| At1g15690/F7H2_3 [Arabidopsis th... 1314 0.0
gi|34894952|ref|NP_908801.1| putative H+-pyrophosphatase [O... 994 0.0
gi|33465893|gb|AAQ19328.1| H+-pyrophosphatase [Oryza sativa... 991 0.0
gi|4126976|dbj|BAA36841.1| vacuolar H+-pyrophosphatase [Cha... 941 0.0
gi|45267862|gb|AAS55761.1| putative inorganic diphosphatase... 937 0.0
gi|2118183|pir||S61425| inorganic diphosphatase (EC 3.6.1.1)... 881 0.0
gi|14970742|emb|CAC44451.1| proton-translocating inorganic ... 833 0.0
gi|1049255|gb|AAA80347.1| H+-pyrophosphatase 815 0.0
gi|21654895|gb|AAK95376.1| vacuolar-type proton translocati... 692 0.0
gi|8886133|gb|AAF80381.1| vacuolar-type proton translocatin... 681 0.0
gi|24214171|ref|NP_711652.1| Pyrophosphate-energized vacuol... 646 0.0
gi|13661740|gb|AAK38077.1| H+-translocating inorganic pyrop... 611 e-173
gi|13661738|gb|AAK38076.1| H+-translocating inorganic pyrop... 610 e-173
gi|23509763|ref|NP_702430.1| V-type H(+)-translocating pyro... 585 e-165
gi|4324984|gb|AAD17215.1| proton-pumping vacuolar pyrophosp... 585 e-165
gi|23483521|gb|EAA19163.1| V-type H(+)-translocating pyroph... 582 e-165

gi|14149007|emb|CAC39165.1| vacuolar-type H+-pyrophosphatas... 570 e-161
gi|28210139|ref|NP_781083.1| vacuolar-type H+-pyrophosphata... 513 e-144
gi|20092675|ref|NP_618750.1| inorganic pyrophosphatase [Met... 483 e-135
gi|33301196|sp|Q8TJA9|HPP1_METAC Pyrophosphate-energized pr... 483 e-135
gi|21226802|ref|NP_632724.1| vacuolar-type H+-pyrophosphata... 482 e-134
gi|5708065|dbj|BAA83103.1| inorganic pyrophosphatase [Aceta... 472 e-131
gi|34762889|ref|ZP_00143872.1| Inorganic pyrophosphatase [F... 457 e-127
gi|19705321|ref|NP_602816.1| Inorganic pyrophosphatase [Fus... 455 e-126
gi|15642948|ref|NP_227989.1| pyrophosphatase, proton-transl... 446 e-123
gi|1076628|pir||S54173 inorganic diphosphatase (EC 3.6.1.1)... 442 e-122
gi|39998380|ref|NP_954331.1| V-type H(+)-translocating pyro... 439 e-121
gi|48845538|ref|ZP_00299816.1| COG3808: Inorganic pyrophosp... 434 e-120
gi|21226803|ref|NP_632725.1| vacuolar-type H+-pyrophosphata... 431 e-119
gi|48838581|ref|ZP_00295523.1| COG3808: Inorganic pyrophosp... 431 e-119
gi|30249887|ref|NP_841957.1| Inorganic H+ pyrophosphatase [... 429 e-118
gi|41723517|ref|ZP_00150444.1| COG3808: Inorganic pyrophosp... 428 e-118
gi|48764244|ref|ZP_00268796.1| COG3808: Inorganic pyrophosp... 427 e-118
gi|33301139|sp|O68460|HPPA_RHORU Pyrophosphate-energized pr... 426 e-118
gi|46201733|ref|ZP_00054472.2| COG3808: Inorganic pyrophosp... 426 e-117
gi|45530368|ref|ZP_00181500.1| COG3808: Inorganic pyrophosp... 425 e-117
gi|33301186|sp|Q8KY01|HPP2_RHOPO Pyrophosphate-energized pr... 420 e-116
gi|22971000|ref|ZP_00018005.1| hypothetical protein [Chloro... 418 e-115
gi|20092676|ref|NP_618751.1| inorganic pyrophosphatase [Met... 418 e-115
gi|20806805|ref|NP_621976.1| vacuolar-type H+-translocating... 416 e-115
gi|27380137|ref|NP_771666.1| H+ translocating pyrophosphate... 416 e-114
gi|29348820|ref|NP_812323.1| pyrophosphate-energized vacuol... 412 e-113
gi|47575275|ref|ZP_00245310.1| COG3808: Inorganic pyrophosp... 408 e-112
gi|21244165|ref|NP_643747.1| H+ translocating pyrophosphate... 408 e-112
gi|15888511|ref|NP_354192.1| AGR_C_2169p [Agrobacterium tum... 403 e-110
gi|17935080|ref|NP_531870.1| H+ translocating pyrophosphate... 402 e-110
gi|15219362|ref|NP_173122.1| vacuolar-type H+-translocating... 402 e-110
gi|42523211|ref|NP_968591.1| vacuolar-type H+-pyrophosphata... 402 e-110
gi|15964971|ref|NP_385324.1| PROBABLE H+ TRANSLOCATING PYRO... 400 e-110
gi|45915706|ref|ZP_00194428.2| COG3808: Inorganic pyrophosp... 399 e-109
gi|25290360|pir||H96818 hypothetical protein F9K20.2 [impor... 397 e-109
gi|13476947|ref|NP_108517.1| H+ translocating pyrophosphate... 397 e-109
gi|18412180|ref|NP_565195.1| vacuolar-type H+-translocating... 396 e-109

gi|6901676|gb|AAF31163.1| vacuolar-type H+-translocating in... 396 e-109
gi|48851197|ref|ZP_00305439.1| COG3808: Inorganic pyrophosp... 395 e-108
gi|21232741|ref|NP_638658.1| H+ translocating pyrophosphate... 393 e-107
gi|48858370|ref|ZP_00312326.1| COG3808: Inorganic pyrophosp... 392 e-107
gi|17987468|ref|NP_540102.1| H+ TRANSLOCATING PYROPHOSPHATE... 390 e-107
gi|23501658|ref|NP_697785.1| V-type H(+)-translocating pyro... 387 e-106
gi|33301205|sp|Q8YGH4|HPPA_BRUME Pyrophosphate-energized pr... 387 e-106
gi|18419442|gb|AAL69328.1| inorganic pyrophosphatase [Bruce... 383 e-105
gi|39935798|ref|NP_948074.1| H+ translocating pyrophosphate... 379 e-103
gi|18419444|gb|AAL69329.1| inorganic pyrophosphatase [Sinor... 377 e-103
gi|23479810|gb|EAA16540.1| vacuolar-type H+ pumping pyropho... 372 e-101
gi|16125612|ref|NP_420176.1| proton pump, putative [Cauloba... 371 e-101
gi|48835222|ref|ZP_00292223.1| COG3808: Inorganic pyrophosp... 347 7e-94
gi|29831159|ref|NP_825793.1| putative inorganic H+ pyrophos... 344 4e-93
gi|18312865|ref|NP_559532.1| vacuolar-type H+-pyrophosphata... 343 7e-93

Alignments

□ >gi|15982958|gb|AAL11507.1| vacuolar H+-pyrophosphatase [Prunus persica]
Length = 759

Score = 1120 bits (2898), Expect = 0.0

Identities = 608/767 (79%), Positives = 662/767 (86%), Gaps = 10/767 (1%)

Query: 5 ALLPELWTEILVPICAVIGIAFSLFQWYVVSRVKLTSDLXXXXXXXXXXXXDYLI-
63

LL E T++L+P+ A++G+AF+L QW++VSRVK++ D LI

Sbjct: 2 GLLSEGLTQLLIPLAALVGLAFALLQWFLVSRVKVSGS-----YGEONGYKDKLIG 52

Query: 64

EEEEGVNDQSVVAKCAEIQTaisegatsflfteykyxxxxxxxxxxxxxxlgsvegfst 123

E EEGV+ V K AEIQ AIS GATsflft+Y+Y LGSV+GFST

Sbjct: 53 EAEEGVDSLEVTIKVAEIQNAISIGATSFLFTQYRYLSIFVGVFSAIIFLFLGSVKGFST
112

Query: 124

DNKPCTYDTRCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKEV 183
++PCTY+T TCKPALA A F+TIAF+LGA+TSVLSGF GMKIATYANARTTLEAR+GV

Sbjct: 113

KSEPCPTYNTGNTCKPALANALFTTIAFLLGALTSGFFGMKIATYANARTTLEARRGV 172

Query: 184

GKAFIVAFRSGAVMGFLAAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSMAL 243
GKAFI AFRSGAVMGFLAA+GLLVLYITIN+FK+YYGDDWEGL+E+ITGYGLGGSSMAL

Sbjct: 173

GKAFTAFRSGAVMGFLAAANGLLVLYITINLFKLYYGDDWEGLYESITGYGLGGSSMAL 232

Query: 244

FGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDFGSY 303

FGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDFGSY

Sbjct: 233

FGRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDFGSY 292

Query: 304 AEASCAALVVASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEIEP
363

AE+SCAAL VASISSFGI+HD+TAM YPL+ISSMGI+VCLITTLFATD FEIK V EIEP

Sbjct: 293 AESSCAALFVASISSFGISHDYTAMSYPかいSSMGIVVCLITTLFATDLFEIKKVNEIEP
352

Query: 364 ALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVKNWQLFLCVCVGLWAGLIG
423

+LK QL+ISTV+MT GIA V++V LP+ FT+F FGT K VKNW LF CV +GLWAGL+IG

Sbjct: 353

SLKRQLLISTVLMTAGIAAVTFVALPSEFTLFQFGTNKAVKNWYLFFCVAIGLWAGLVIG 412

Query: 424

FVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXX 483
+ TEY+TSNAYSPVQDVADSCRTGAATNVIFGLALGYK M

Sbjct: 413 YTTEYHTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIIPVFAIAFAIYVSFSLAAM
472

Query: 484

YGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTAAI 543
YG+AVAALGMLSTI+TGLAIDAYGPISDNAGGIAEMAGMSH IRERTDALDAAGNTAAI
Sbjct: 473 YGIAVAALGMLSTISTGLAIDAYGPISDNAGGIAEMAGMSHEIRERTDALDAAGNTAAI
532

Query: 544

GKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAML PYWFSAMTMKSVGS 603
GKGFAIGSAALVSLALFGA+VSRAGI TVDVLTPKVIIGLLVGAML PYWFSAMTMKSVGS
Sbjct: 533

GKGFAIGSAALVSLALFGAYVSRAGIETVDVLTPKVIIGLLVGAML PYWFSAMTMKSVGS 592

Query: 604

AALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFF 663
AALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDAS+KEMIPPG LVMLTPLI G F
Sbjct: 593

AALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASLKEMIPPGALVMLTPLIAGTF 652

Query: 664

FGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHKAA 723
FGVETL+G+LAGSLVSGVQIAISASNTGGAWDNAKKYIEAG SEHAKSLGPKGS+PHKAA
Sbjct: 653

FGVETLAGILAGSLVSGVQIAISASNTGGAWDNAKKYIEAGASEHAKSLGPKGSDPHKAA 712

Query: 724 VIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

VIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFA HGG+LFK+
Sbjct: 713 VIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFAAHGGVLFKWL 759



>gi|3298474|dbj|BAA31523.1| ovp1 [Oryza sativa]

Length = 771

Score = 1167 bits (3019), Expect = 0.0

Identities = 633/769 (82%), Positives = 674/769 (87%), Gaps = 3/769 (0%)

Query: 5 ALLPELWTEILVPICAVIGIAFSLFQWYVVSRVKLTSDLXXXXXXXXXXXXXX--DY

61

A+LP+L T++LVP AV+GIAF++ QW +VS+VK+T++ +Y

Sbjct: 3

AILPDLATQVLVPAAAVVIAFAVVQWVLVSKVKMTAERRGGEGSPGAAAGKDGGAASEY 62

Query: 62

LIEEEEGVNDQSVVAKCAEIQTAISEGATSFLFTEYKYXXXXXXXXXXXXXLSVGSVEGF 121

LIEEEEG+N+ +VV KC+EIQ AISEGATSFLFTEYKY LGSVEGF

Sbjct: 63 LIEEEGLNEHNVVEKCSEIQHAISEGATSFLFTEYKYVGLFMGIFAVLIFLFLGSVEGF

122

Query: 122

STDNKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVSGFLGMKIATYANARTTLEARK 181

ST ++PC Y R CKPALA A FST+AFVLGAVTS++SGFLGMKIATYANARTTLEARK

Sbjct: 123

STKSQPCHYSKDRMCKPALANAIFSTVAFVLGAVTSVSGFLGMKIATYANARTTLEARK 182

Query: 182

GVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSM 241

GVGKAFI AFRSGAVMGFLLAASGL+VLYI IN+F IYYGDDWEGLFEAITGYGLGGSSM

Sbjct: 183

GVGKAFITAFRSGAVMGFLLAASGLVLYIAINLFGIYYGDDWEGLFEAITGYGLGGSSM 242

Query: 242

ALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAPIADNVGDNVGDIAGMGSDLFG 301

ALFGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAPIADNVGDNVGDIAGMGSDLFG

Sbjct: 243

ALFGRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAPIADNVGDNVGDIAGMGSDLFG 302

Query: 302 SYAEASCAALVVASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEI

361

SYAE+SCAALVVASISSFGINH+FT M YPLLISS+GI+ CLITTLFATDFFEIK V EI

Sbjct: 303 SYAESSCAALVVASISSFGINHEFTPMLYPLLISSVGIIACLITTLFATDFFEIKAVDEI 362

Query: 362

EPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGLI 421

EPALK QLIISTV+MTVGI +VSW+GLP SFTIFNFG QK V NWQLFLCV VGLWAGLI

Sbjct: 363

EPALKKQLIISTVVMTVGIVLVSWLGLPYSFTIFNFGAQKTVYNWQLFLCVAVGLWAGLI 422

Query: 422

IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXX 481

IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 423 IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAFSIFLSFSLA
482

Query: 482

XMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTTA 541

MYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTTA

Sbjct: 483

AMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTTA 542

Query: 542

AIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKSV 601

AIGKGFAIGSAALVSLALFGAFVSRAITVDVLTPKVIIGLLVGAMLPYWFSAMTMKSV

Sbjct: 543

AIGKGFAIGSAALVSLALFGAFVSRAAISTVDVLTPKVFIGLIVGAMLPYWFSAMTMKSV 602

Query: 602

GSAALKMVEVRRQFNTPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVG 661

GSAALKMVEVRRQFN+IPGLMEGT KPDYATCVKISTDASIKEMIPPG LVML+PLIVG

Sbjct: 603

GSAALKMVEVRRQFNIPGLMEGTTKPDYATCVKISTDASIKEMIPPGALVMLSPLIVG 662

Query: 662

FFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHK 721

FFGVETLSG+LAG+LVSGVQIAISASNTGGAWDNAKKYIEAG SEHA++LGPKGS+ HK

Sbjct: 663

IFFGVETLSGLLAGALVSGVQIAISASNTGGAWDNAKKYIEAGASEHARTLGPKGSDCHK 722

Query: 722 AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFK+F

Sbjct: 723 AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKWF 771

>gi|2129950|pir||S61423 inorganic diphosphatase (EC 3.6.1.1) (clone TVP9) - common tobacco

Length = 765

Score = 1194 bits (3088), Expect = 0.0

Identities = 647/769 (84%), Positives = 683/769 (88%), Gaps = 4/769 (0%)

Query: 2 VAPALLPELWTEILVPICAVIGIAFSLFQWYVVSRVKLTSDLXXXXXXXXXXXXDY

61

+ ALLP+L EI++P+CAVIGI FSL QWY+VS VKLT + DY

Sbjct: 1 MGAALLPDLGAEIVIPVCAVIGIVFSLVQWYLVSNVKLTPE----SSPSNNGKNGYGDY

56

Query: 62

LIEEEEGVNDQSVVAKCAEIQTAISEGATSFLFTEYKYXXXXXXXXXXXXLGSVEGF 121

LIEEEEG+N+Q+VV KCAEIQ AISEGATSFLFT Y+Y LGSVEGF

Sbjct: 57 LIEEEEGINEQNVVVKCAEIQNAISEGATSFLFTTYQYVGIFMIAFAILIFLFLGSVEGF

116

Query: 122

STDNKPCTYDTRRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARK 181

ST ++PCTY+ + CKPALATA FST++F+LGAVTSV+SGFLGMKIATYANARTTLEARK

Sbjct: 117

STKSQPCTYNKEKLCKPALATAIFSTVSFLLGAVTSVSGFLGMKIATYANARTTLEARK 176

Query: 182

GVGKAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSM 241

GVGKAFIVAFRSGAVMGFLAA+GLLVLYI IN+FK+YYGDDWEGLFEAITGYGLGGSSM

Sbjct: 177

GVGKAFIVAFRSGAVMGFLLAANGLLVLYIAINLFKLYYGDDWEGLFEAITGYGLGGSSM 236

Query: 242

ALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAFMGSDFLG 301

ALFGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAFMGSDFLG

Sbjct: 237

ALFGRVGGGIYTKAADVGADLVGVERNIPEDDPRNPAVIADNVGDNVGDIAFMGSDFLG 296

Query: 302 SYAEASCAALVVASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEI

361

SYAEASCAALVVASISSFGINH+FTAM YPLLISSMGIL+CLITTLFATDFFEIK VKEI

Sbjct: 297 SYAEASCAALVVASISSFGINHEFTAMLYPLLISSMGILICLITTLFATDFFEIKAVKEI 356

Query: 362

EPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVVGLWAGLI 421

EPALKNQLIIST +MTVGIAIV+W LP+SFTIFNFG QKVVKNWQLFLCV VGLWAGLI

Sbjct: 357 EPALKNQLIISTALMTVGIAIVWTCLPSSFTIFNFGAQKVVKNWQLFLCVAVGLWAGLI

416

Query: 422

IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXX 481

IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGY

Sbjct: 417 IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAIAIFVSFSFA

476

Query: 482

XMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTA 541

M +AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTA

Sbjct: 477

AMGYIAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTA 536

Query: 542

AIGKGFAIGSAALVSLALFGAFVSRAIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKSV 601

AIGKGFAIGSAALVSLALFGAFVSRAI TVDVLTP+V IGL+VGAMLPYWFSAMTMKSV

Sbjct: 537

AIGKGFAIGSAALVSLALFGAFVSRAIITVDVLTPQVFIGLIVGAMLPYWFSAMTMKSV 596

Query: 602

GSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVG 661
GSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPG LVMLTPLIVG

Sbjct: 597

GSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGALVMLTPLIVG 656

Query: 662

FFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHK 721

FFGVETLSGVLAG+LVSGVQIAISASNTGGAWDNAKKYIEAG SEHA++LGPKGS+PHK

Sbjct: 657

IFFGVETLSGVLAGALVSGVQIAISASNTGGAWDNAKKYIEAGASEHARTLGPKGSDPHK 716

Query: 722 AAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

AAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGG+LFK F

Sbjct: 717 AAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGLLFKIF 765



>gi|15982956|gb|AAL11506.1| vacuolar H+-pyrophosphatase [Prunus persica]

Length = 767

Score = 1186 bits (3068), Expect = 0.0

Identities = 645/765 (84%), Positives = 682/765 (89%), Gaps = 1/765 (0%)

Query: 6 LLPELWTEILVPICAVIGIAFSLFQWYVVSRVKLTSDLXXXXXXXXXXXXXXDYLIEE
65

LL L TEI++P+ AVIGI FSL QW++VSrvk+T + DYLIEE

Sbjct: 4 LLSTLATEIVIPVAAVIGIVFSLVQWFIVSRVKVTLE-RHAPPAGPNSNKNGFNDYLIIEE 62

Query: 66

EEGVNDQSVVAKCAEIQTaisegatsflfteykyxxxxxxxxxxxxxxlgsvegfstdn 125

EEG++DQ+VVAKCAEIQ AISEGATSFLFTEY+Y LGsvegfst +

Sbjct: 63 EEGLHDQNVVAKCAEIQNaisegatsflfteyqyvgvfmvvfailiflflgsvegfstks

122

Query: 126

KPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGVGK 185
+PCTYD RTCKPALATA FST+AFVLG VTS+LSGFLGMKIATYANARTTLEARKGVGK

Sbjct: 123

QPCTYDAQRTCKPALATAIFSTVAFLGGVTSILSGFLGMKIATYANARTTLEARKGVGK 182

Query: 186

AFIVAFRSGAVMGFLAAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSMALFG 245
AFIVAFRSGAVMGFLAA+GLLVLYITINVFK+YYGDDWEGLFE+ITGYGLGGS+MALFG

Sbjct: 183

AFIVAFRSGAVMGFLAANGLLVLYITINVFKVYYGDDWEGLFESITGYGLGGSAMALFG 242

Query: 246

RVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAE 305

RVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAE

Sbjct: 243

RVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAE 302

Query: 306 ASCAALVVASISSFGINHDFTAMCYPLLISSMGLVCLITTLFATDFFEIKLVKEIEPAL
365

+SCAALVVASISSFGINH+FT+M YPLLISSMGL+CLITTLFATDFFEIK VKEIEPAL

Sbjct: 303 SSCAALVVASISSFGINHEFTSMLYPPLIISSMGILICLITTLFATDFFEIKAVKEIEPAL 362

Query: 366 KNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGLIIGFV
425

K QLIISTV+MTVGIAI+SW+ LP+SFTI+NFG QKVVKNWQLFLCV VGLWAGLIIGFV

Sbjct: 363 KKQLIISTVLMVTGIAISWIALPSSFTIYNFGVQKVVKNWQLFLCVAVGLWAGLIIGFV
422

Query: 426

TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXXMYG 485

TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK MYG

Sbjct: 423 TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSIIPIFAIAVSIFVSFSFAAMYG
482

Query: 486

VAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTAAIGK 545
+AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTAAIGK

Sbjct: 483

IVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTAAIGK 542

Query: 546

GFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKSVGSAA 605

GFAIGSAALVSLALFGAFVSRA I TVDVLT PKV IGL+VGAMLP FSAMTMKSVGSAA

Sbjct: 543

GFAIGSAALVSLALFGAFVSRAAISTVDVLTPKVFIGLIVGAMLPTGFSAMTMKSVGSAA 602

Query: 606

LKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFFF 665

LKMVEEVRRQFNTIPGLMEGTAKP YATCVKISTDASIKEMIPPG LV+LTPLIVG FG

Sbjct: 603 LKMVEEVRRQFNTIPGLMEGTAKPSYATCVKISTDASIKEMIPPGALVLTPLIVGTLFG
662

Query: 666

VETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHKAAVI 725

VETLSGVLAGSLVSGVQ+AISASNTGGAWDNAKKYIEAG SEHA++LGPKGS+PHKAAVI

Sbjct: 663

VETLSGVLAGSLVSGVQVAISASNTGGAWDNAKKYIEAGASEHARTLGPKGSDPHKAAVI 722

Query: 726 GDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

GDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGG+LFK F

Sbjct: 723 GDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGLLFKIF 767

>gi|38488588|dbj|BAD02276.1| vacuolar proton pyrophosphatase [Oryza sativa (japonica
cultivar-group)]

Length = 762

Score = 1144 bits (2958), Expect = 0.0

Identities = 621/766 (81%), Positives = 667/766 (87%), Gaps = 5/766 (0%)

Query: 5 ALLPELWTEILVPIAVIGIAFSLFQWYVVSRVKLTSDLXXXXXXXXXXXXXXDYLIE
64

A+L ++ TE+L+PI A+IGI FS+ QW +V+RVKL D LIE

Sbjct: 2 AILSDVATEVLIPIAIIIGIGFSIAQWVLVARVKLAPS----QPGASRSKDGYGDSLIE 56

Query: 65

EEEGVNDQSVVAKCAEIQTASEGATSFLTEYKYXXXXXXXXXXXXXLSVEGFSTD 124

EEEG+ND +VVAKCAEIQ AI+EGATSFLFTEY+Y LGSVEGFST

Sbjct: 57 EEEGLNDHNVVAKCAEIQNIAEAGATSFLFTEYQYVGVFMSIFAVVIFLFLGSVEGFSTK
116

Query: 125

NKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGVG 184

PCTY + CKPAL A FST++F+LGA+TSV+SGFLGMKIATYANARTTLEARKGVG

Sbjct: 117

THPCTYSKDKECKPALFNALFSTVSFLLGAITSVSGFLGMKIATYANARTTLEARKGVG 176

Query: 185

KAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEITGYGLGGSSMALF 244

KAFI AFRSGAVMGFLA++GLLVLYI IN+FK+YYGDDWEGLFE+ITGYGLGGSSMALF

Sbjct: 177

KAFITAFRSGAVMGFLASNGLLVLYIAINLFKMYYGDDWEGLFESITGYGLGGSSMALF 236

Query: 245

GRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAPIADNVGDNVGDIAGMGSDFGSYA 304

GRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAPIADNVGDNVGDIAGMGSDFGSYA

Sbjct: 237

GRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAPIADNVGDNVGDIAGMGSDFGSYA 296

Query: 305 EASCAALVVASISSFGINHDFTAMCYPLLISSMGLVCLITTLFATDFFEIKLVKEIEPA

364

E+SCAALVVASISSFGINHDFT MCYPLL+SSMGI+VCLITTLFATDFFEIK VKEIEP+

Sbjct: 297 ESSCAALVVASISSFGINHDFTGMCYPLLVSSMGIIVCLITTLFATDFFEIKAVKEIEPS

356

Query: 365 LKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVGLWAGLIIGF
424

LK QLIIST +MTVGIA+VSW+ LP FTIFNFG QK V NW LFLCV +GLWAGLIIG+

Sbjct: 357 LKKQLIISTALMTVGIALVSWLALPYKFTIFNFGEQKEVTNWGLFLCVSIGLWAGLIIGY
416

Query: 425

VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXMY 484

VTEYYTSNAYSPVQDVAD+CRTGAATNVIFGLALGYK MY

Sbjct: 417 VTEYYTSNAYSPVQDVADACRTGAATNVIFGLALGYKSIIPIFAIALGIYVSFTIAAMY
476

Query: 485

GVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTAAIG 544

G+AVAALGMLSTIATGL+IDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTAAIG

Sbjct: 477

GINVAALGMLSTIATGLSIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTAAIG 536

Query: 545

KGFAIGSAALVSLALFGAFVSRAFIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKSVGSA 604

KGFAIGSAALVSLALFGAFVSRAF+ VDVL+PKVIIGL+VGAMLPYWFSAMTMKSVGSA

Sbjct: 537

KGFAIGSAALVSLALFGAFVSRAFKVVDVLSPKVIIGLIVGAMLPYWFSAMTMKSVGSA 596

Query: 605

ALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFFF 664

ALKMVEEVRRQFNTIPGLMEGT KPDYA CVKISTDASIK+MIPPG LVMLTPLIVG F

Sbjct: 597

ALKMVEEVRRQFNTIPGLMEGTGKPDYANCVKISTDASIKQMIPPGALVMLTPLIVGTLF 656

Query: 665

GVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHKAAV 724

GV+TLSGVLAG+LVSGVQ+AISASNTGGAWDNAKKYIEAG SEHA+SLGPKGS+ HKAAV

Sbjct: 657

GVQTLSGVLAGALVSGVQVAISASNTGGAWDNAKKYIEAGASEHARSLGPKGSDCHKAAV 716

Query: 725 IGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

IGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFK F
Sbjct: 717 IGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKLF 762

>gi|322841|pir||JC1466 inorganic diphosphatase (EC 3.6.1.1) - barley
Length = 761

Score = 1154 bits (2985), Expect = 0.0
Identities = 624/765 (81%), Positives = 671/765 (87%), Gaps = 6/765 (0%)

Query: 5 ALLPELWTEILVPICAVIGIAFSLFQWYVVSRVKLTSDLXXXXXXXXXXXXXXDYIE
64

A+L EL TEIL+P+C VIGI F++ QW++VS+VK+T DYIE
Sbjct: 2 AILGELGTEILIPVCVGIVFAVAQWFIVSKVKVTP----GALRRRAKNGYGDYIE 56

Query: 65
EEEGVNDQSVVAKCAEIQTASEGATSFLTEYKYXXXXXXXXXXXXXLSVEGFSTD 124
EEEG+ND +VV KCAEIQTASEGATSFLFT Y+Y LGS+EGFST
Sbjct: 57 EEEGLNDHNVVVKCAEIQTASEGATSFLFTMYQYVGMFMVVFAAIIFLFLGSIEGFSTK
116

Query: 125
NKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGVG 184
+PCTY + TCKPAL TA FST +F+LGA+TS++SGFLGMKIATYANARTTLEARKGVG
Sbjct: 117 GQPCTY-
SKGTCKPALYTALFSTASFLLGAITSVSGFLGMKIATYANARTTLEARKGVG 175

Query: 185
KAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSMALF 244
KAFI AFRSGAVMGFL++SGL+VLYITINVFK+YYGDDWEGLFE+ITGYGLGGSSMALF
Sbjct: 176
KAFITAFRSGAVMGFLSSSGLVLYITINVFKMYYGDDWEGLFESITGYGLGGSSMALF 235

Query: 245
GRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAPIADNVGDNVGDAGMGSDFGSYA 304

GRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAFMGSDFGSYA

Sbjct: 236

GRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAFMGSDFGSYA 295

Query: 305 EASCAALVVASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEIEPA
364

E+SCAALVVASISSFGINHDFTAMCYPLL+SS+GI+VCL+TTLFATDFFEIK EIEPA

Sbjct: 296 ESSCAALVVASISSFGINHDFTAMCYPLLVSSVGIIVCLLTLFATDFFEIKAAANEIEPA
355

Query: 365 LKNQLIISTVIMTVGIAIVSWGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGLIIGF
424

LK QLIIST +MTVG+A++SW+ LP FTIFNFG QK V NW LF CV VGLWAGLIIGF

Sbjct: 356 LKKQLIISTALMTGVAVISWLALPAKFTIFNFGAQKEVSNWGLFFCVAVGLWAGLIIGF
415

Query: 425

VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXMY 484

VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK MY

Sbjct: 416 VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSIIPIFAIAVSIYVSFSIAAMY
475

Query: 485

GVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTAAIG 544

G+A+AALGMLST+ATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTAAIG

Sbjct: 476

GIAMAALGMLSTMATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTAAIG 535

Query: 545

KGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKSVGSA 604

KGFAIGSAALVSLALFGAFVSrag+ VDVL+PKV IGL+VGAMLPYWFSAMTMKSVGSA

Sbjct: 536

KGFAIGSAALVSLALFGAFVSRAVGKVVDVLSPKVFIGLIVGAMLPYWFSAMTMKSVGSA 595

Query: 605

ALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEIMPAGCLVMLTPLIVGFFF 664

ALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPG LVMLTPLIVG F
Sbjct: 596

ALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGALVMLTPLIVGTLF 655

Query: 665

GVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHKA AV 724
GVETLSGVLAG+LVSGVQIAISASNTGGAWDNAKKYIEAG SEHA+SLGPKGS+ HKAAV

Sbjct: 656

GVETLSGVLAGALVSGVQIAISASNTGGAWDNAKKYIEAGNSEHARSLGPKGSDCHKA AV 715

Query: 725 IGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKY 769

IGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFAT+GG+LFKY

Sbjct: 716 IGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATYGGLLFKY 760

>gi|3608171|dbj|BAA33149.1| proton-translocating inorganic pyrophosphatase [Cucurbita moschata]

Length = 768

Score = 1182 bits (3058), Expect = 0.0

Identities = 638/765 (83%), Positives = 676/765 (88%), Gaps = 1/765 (0%)

Query: 6 LLPELWTEILVPICAVIGIAFSLFQWYVVSRVKLTSDLXXXXXXXXXXXXXXDYLIEE
65

+LP+L TEI +P+CAVIGI FSL QWY VS+VKL+ DYLIEE

Sbjct: 5 ILPDLGTEIFIPVCAVIGIVFSLVQWYYVSQVKLSPG-RDAAHNN SAGSKNGYSDYLI EEE
63

Query: 66

EEGVNDQSVVAKCAEIQT AISEGATSFLFTEYKYXXXXXXXXXXXXXLSVEGFSTD N 125

EEGVND +VV KCAEIQ+AISEGATSFLFTEYKY LG SVE FST

Sbjct: 64 EEEGVNDHN VVVIKCAEIQS AISEGATSFLFTEYKYVGIFMVLF A VLIFVFLGSV E SFSTKP
123

Query: 126

KPCTYDTRTRCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGVGK 185
+PCTYD TRTCKPALATA FST++F+LGAVTSV+SGFLGMKIATYANARTTLEARKGVGK

Sbjct: 124

QPCTYDKTRTRCKPALATAIFSTVSFLGAVTSVSGFLGMKIATYANARTTLEARKGVGK 183

Query: 186

AFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSMALFG 245

AFI AFRSGAVMGFLAA+GLLVL+I IN+FK+YYGDDW GLFE+ITGYGLGGSSMALFG

Sbjct: 184

AFITAFRSGAVMGFLAANGLLVLFIAINLFKLYYGDDWGGLFESITGYGLGGSSMALFG 243

Query: 246

RVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAE 305

RVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAE

Sbjct: 244

RVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAE 303

Query: 306 ASCAALVVASISSFGINHDFTAMCYPLLISSMGLVCLITTLFATDFFEIKLVKEIEPAL
365

+SCAALVVASIS FG NH+ T M YPL++SSMGLVCLITTLFATDFFEIK VKEIEPAL

Sbjct: 304 SSCAALVVASISPGNHELTPMLYPLIVSSMGLVCLITTLFATDFFEIKAVKEIEPAL
363

Query: 366 KNQLIISTVIMTVGIAIVSWGLPTSFTIFNFGTQKVVKNWQLFLCVCGWLWAGLIIGFV
425

K QLIISTV+MT GIAIV+W+ +P+SFTIFNFGTQKV NW+LFLCV VGLWAGLIIGFV

Sbjct: 364 KKQLIISTVLMTFGIAIVTWLSVPSSFTIFNFGTQKVVTNWKLFLCVAVGLWAGLIIGFV
423

Query: 426

TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXMYG 485

TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK MYG

Sbjct: 424 TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSIIPIFAIAVSIFVSFTAAMYG
483

Query: 486

VAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTAAIGK 545
+AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTAAIGK

Sbjct: 484

IAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTAAIGK 543

Query: 546

GFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKSVGSAA 605
GFAIGSAALVSLALFGAFVSRA+ VDVLTPKV IGL+VGAMLPYWFSAMTMKSVGSAA

Sbjct: 544

GFAIGSAALVSLALFGAFVSRAGVTAVDVLTPKVFIGLIVGAMLPYWFSAMTMKSVGSAA 603

Query: 606

LKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFFF 665
LKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPG LVMLTPLIVG FG
Sbjct: 604 LKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGALVMLTPLIVGILFG
663

Query: 666

VETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHKAAVI 725
VETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAG S+HA++LGPKGS+PHKAAVI

Sbjct: 664

VETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGASKHARTLGPKGSDPHKAAVI 723

Query: 726 GDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

GDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFA+HGG+LFK F
Sbjct: 724 GDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFASHGGLLFKIF 768

► >gi|7436046|pir||T14563 inorganic diphosphatase (EC 3.6.1.1) - beet
gi|485742|gb|AAA61609.1| pyrophosphatase [Beta vulgaris]

Length = 761

Score = 1202 bits (3109), Expect = 0.0

Identities = 646/765 (84%), Positives = 685/765 (89%), Gaps = 4/765 (0%)

Query: 6 LLPELWTEILVPICAVIGIAFSLFQWYVSRVKLTSDLXXXXXXXXXXXXXXDYLIEE
65

++ +L TEI +P+CAVIG S +QW++VS+VK+++D DYLIEE

Sbjct: 1 MISDLATEIFIPVCAGIVY-ISCYQWFLVSKVKSTD---RHVNNGGSAKNGFNDYLIEE 56

Query: 66

EEGVNDQSVAKCAEIQTASEGATSFLTEYKYXXXXXXXXXXXXXLSVEGFSTDN 125

EEGVNDQ+WAKCAEIQAISEGATSFLTEY+Y LGSVEGFST++

Sbjct: 57

EEGVNDQNVAKCAEIQNASEGATSFLTEYQYVGVMCAFAVLIFVFLGSVEGFSTES 116

Query: 126

KPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGVGK 185

+PCTY + CKPALATA FST++F+LGA+TSV+SGFLGMKIAT ANARTTLEARKGVGK

Sbjct: 117

QPCTYSPLKKCKPALATALFSTVSFLLGAITSVSGFLGMKIATDANARTTLEARKGVGK 176

Query: 186

AFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSMALFG 245

AFI+AFRSGAVMGFLAA+GLLVLYI IN+ K+YYGDDWEGLFEAITGYGLGGSSMALFG

Sbjct: 177

AIIIAFRSGAVMGFLAANGLLVLYIAINLLKLYYGDDWEGLFEAITGYGLGGSSMALFG 236

Query: 246

RVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAE 305

RVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAE

Sbjct: 237

RVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAE 296

Query: 306 ASCAALVVASIISSGINHDFTAMCYPLLISSMGIILVCLITLFAFDFFIEIKLVKEIEPAL

365

ASCAALVVASIISSGINH+FTAMCYPLLISSMGI+VCL+TTLFAFDFFIEIK VKEIEPAL

Sbjct: 297 ASCAALVVASIISSGINHEFTAMCYPLLISSMGIIVCLVTTLFATDFFIEIKAVKEIEPAL

356

Query: 366 KNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKWQLFLCVCVGLWAGLIIGFV
425

K QLIISTV+MTVGIAI++W+ LP+SFTIFNFGTQKVW NWQLFLCVCVGLWAGLIIGFV

Sbjct: 357 KKQLIISTVLMVTVGIAITWIALPSSFTIFNFGTQKVWHNWQLFLCVCVGLWAGLIIGFV
416

Query: 426

TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXMYG 485

TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK MYG

Sbjct: 417 TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSIIPIFAIAVSIFVSFSFAAMYG
476

Query: 486

VAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTAAIGK 545

VAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTAAIGK

Sbjct: 477

VAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTAAIGK 536

Query: 546

GFAIGSAALVSLALFGAFVSRAI TVDVLTPKVIIGLLVGAMLPYWFSAMTMKSVGSAA 605

GFAIGSAALVSLALFGAFVSRAI TVDVLTPKVIIGLLVGAMLPYWFSAMTMKSVGSAA

Sbjct: 537

GFAIGSAALVSLALFGAFVSRAI TVDVLTPKVFIGLIVGAMLPYWFSAMTMKSVGSAA 596

Query: 606

LKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFFF 665

LKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPG LVMLTPLIVG FFG

Sbjct: 597 LKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGALVMLTPLIVGIFFG
656

Query: 666

VETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHKAAVI 725

VETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAG SEHA+SLGPKGSEPHKAAVI

Sbjct: 657

VETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGASEHARSLGPKGSEPHKAAVI 716

Query: 726 GDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

GDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGG+LFK F
Sbjct: 717 GDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGLLFKL 761

>gi|2129948|pir||S61424 inorganic diphosphatase (EC 3.6.1.1) (clone TVP31) - common tobacco

Length = 766

Score = 1172 bits (3032), Expect = 0.0
Identities = 639/770 (82%), Positives = 684/770 (88%), Gaps = 4/770 (0%)

Query: 1

MVAPALLPELWTEILVPICAVIGIAFSLFQWYVVSRVKLTSDLXXXXXXXXXXXXXXD 60
M AP +L +L TEIL+P+CAV+GIAFSLFQW++VS+V L++D +
Sbjct: 1 MGAP-ILSDLGTEILIPVCAVVGIAFSLFQWFLVSKVTL SAD---KSSGAADDKNGYAAE 56

Query: 61

YLIEEEEGVNDQS VVAKCAEIQT ASEGAT SFLFTEY KYXXXXXXXXXXXXX LGSVEG 120
LIEEEEG+ND +VV KCAEIQ AISEGAT SFLFTEY+Y LGSVEG
Sbjct: 57 SLIEEEEGINDHN VVQKCAEIQNA ISEGAT SFLFTEY QYVGFMVAFAILIFL LGSVEG
116

Query: 121

FSTDNK PCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEAR 180
FST N+PCTYD+T+TCKPALATA FST++F+LGAVTSV+SGFLGMKIATYANARTTLEAR
Sbjct: 117
FSTKNQPCTYDSTKTCKPALATAVFSTVSFLGAVTSVSGFLGMKIATYANARTTLEAR 176

Query: 181

KGVGKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS 240
KGVGKAFIVAFRSGAVMGFLAA+GLLVLYITI +FK+YYGDDWEGLFEAITGYGLGGSS
Sbjct: 177
KGVGKAFIVAFRSGAVMGFLAANGLLVLYITILLFKLYYGDDWEGLFEAITGYGLGGSS 236

Query: 241

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAPIADNVGDNVGDIA GMGSDFL 300
MALFGRV GGIYTKAADVGADLVGK+ERNIPE DDPRNPAVIADNVGDNVGDIA GMGSDFL

Sbjct: 237

MALFGRVAGGIYTKAADVGADLVGKVERNIPEDDPRNPAPIADNVGDNVGDIA GMGSDFL 296

Query: 301 GS YAEASCAALVVASI SFGINHDFTAMCYPLI SSMGILVCLITLFATDFFEIKLVKE
360

GS YAE+SCAALVVASI SFG+NH+FTAM YPLL+SS+GILVCL+TTLFATDFFE+K VKE

Sbjct: 297

GS YAE SCAALVVASI SFGVNHEFTAMLYPLL VSSVGILVCLITLFATDFFEVKAVKE 356

Query: 361

IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCV CGVLWAGL 420

IEPALK QL+IST +MTVGIA+V+W+ LP+ FTIFNFG QK VK+WQLFLCV VGLWAGL

Sbjct: 357 IEPALKQQLVISTALMTVGIAVVTWIALPSIFTIFNFGAQKEVKS WQLFLCV CGVLWAGL
416

Query: 421

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXX 480

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 417 IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAVSIFVSFSF
476

Query: 481

XXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTT 540

M +AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTT

Sbjct: 477

AAMGYIAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTT 536

Query: 541

AAIGKGFAIGSAALVSLALFGAFVSRA GIHTVDVLTPKVIIGLLVGAML PYWFSAMTMKS 600

AAIGKGFAIGSAALVSLALFGAFVSRA I TVDVLTPKV IGL+VGAML PYWFSAMTMKS

Sbjct: 537

AAIGKGFAIGSAALVSLALFGAFVSRAAISTVDVLTPKVFIGLIVGAML PYWFSAMTMKS 596

Query: 601

VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIIPPGLVMLTPLIV 660

VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMI PG LVMLTPLIV

Sbjct: 597

VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIAPGALVMLTPLIV 656

Query: 661

GFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPH 720

G FGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA++LGPKGS+ H

Sbjct: 657

GILFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHARTLGPKGSDAH 716

Query: 721 KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGG+LFK F

Sbjct: 717 KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGLLFKLF 766



>gi|1103712|emb|CAA58700.1| inorganic pyrophosphatase [Nicotiana tabacum]

Length = 766

Score = 1180 bits (3053), Expect = 0.0

Identities = 641/770 (83%), Positives = 686/770 (89%), Gaps = 4/770 (0%)

Query: 1

MVAPALLPELWTEILVPICAVIGIAFSLFWYVVSRVKLTSDLXXXXXXXXXXXXXD 60

M AP +L +L TEIL+P+CAV+GIAFSLFW++VS+V L++D +

Sbjct: 1 MGAP-ILSDLGTEILIPVCVVGIAFSLFWFLVSKVTLAAD---KSSGAADDKNGYAAE 56

Query: 61

YLIEEEEGVNDSVVAKCAEIQTASEGATSFLTEYKYXXXXXXXXXXXXXXLGSVEG 120

LIEEEEG+ND +VV KCAEIQ AISEGATSFLTEY+Y LGSVEG

Sbjct: 57 SLIEEEEGINDHNVVQKCAEIQNASEGATSFLTEYQYVGFMVAFAILIFLFLGSVEG

116

Query: 121

FSTDNKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTLEAR 180
FST N+PCTYD+T+TCKPALATA FST++F+LGAVTSV+SGFLGMKIATYANARTLEAR

Sbjct: 117

FSTKNQPCPTYDSTKTCKPALATAVFSTVSFLLGAVTSWSGFLGMKIATYANARTLEAR 176

Query: 181

KGVGKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS 240
KGVGKAFIVAFRSGAVMGFLAA+GLLVLYITI +FK+YYGDDWEGLFEAITGYGLGGSS

Sbjct: 177

KGVGKAFIVAFRSGAVMGFLAANGLLVLYITILLFKLYYGDDWEGLFEAITGYGLGGSS 236

Query: 241

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDF 300
MALFGRV GGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDF

Sbjct: 237

MALFGRVAGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDF 296

Query: 301 GSYAEASCAALVVASISSFGINHDFTAMCYPLLISSMGILVCLITLFATDFFEIKLVKE
360

GSYAE+SCAALVVASISSFG+NH+FTAM YPLL+SS+GILVCL+TTLFATDFFE+K VKE

Sbjct: 297

GSYAESSCAALVVASISSFGVNHEFTAMLYPLLVSSVGILVCLLTLFATDFFEVKAVKE 356

Query: 361

IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCGWLWAGL 420

IEPALK QL+IST +MTVGIA+V+W+ LP+ FTIFNFG QK VK+WQLFLCV VGLWAGL

Sbjct: 357 IEPALKQQLVISTALMTVGIAVVTWIALPSIFTIFNFGAQKEVKSQFLCVGVGLWAGL
416

Query: 421

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXX 480

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 417 IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAVSIFVSFSF
476

Query: 481

XXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTT 540
MYG+AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTT

Sbjct: 477

AAMYGIAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTT 536

Query: 541

AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKS 600

AAIGKGFAIGSAALVSLALFGAFVSRA I TVDVLTPKV IGLLVGAMLPYWFSAMTMKS

Sbjct: 537

AAIGKGFAIGSAALVSLALFGAFVSRAAISTVDVLTPKFIGLLVGAMLPYWFSAMTMKS 596

Query: 601

VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIIPPGLVMLTPLIV 660

VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMI PG LVMLTPLIV

Sbjct: 597

VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIAPGALVMLTPLIV 656

Query: 661

GFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPH 720

G FGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA++LGPKGS+ H

Sbjct: 657

GILFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHARTLGPKGSDAH 716

Query: 721 KAAVIGDTIGDPLKDTGPSLNILIKLMAVESL VFAPFFATHGGILFKYF 770

KAAVIGDT+GDPLKDTGPSLNILIKLMAVESL VFAPFFATHGG+LFK F

Sbjct: 717 KAAVIGDTVGDPDKDTGPSLNILIKLMAVESL VFAPFFATHGGLLFKLF 766

>[gi|7436041|pir|S72526](#) inorganic diphosphatase (EC 3.6.1.1), H⁺-translocating, vacuolar membrane (clone OVP1) - rice
[gi|1747294|dbj|BAA08232.1](#) vacuolar H⁺-pyrophosphatase [Oryza sativa (japonica cultivar-group)]
Length = 771

Score = 1169 bits (3023), Expect = 0.0

Identities = 634/769 (82%), Positives = 675/769 (87%), Gaps = 3/769 (0%)

Query: 5 ALLPELWTEILVPICAVIGIAFSLFQWYVVSRVKLTSDLXXXXXXXXXXXXXX--DY

61

A+LP+L T++LVP AV+GIAF++ QW +VS+VK+T++ +Y

Sbjct: 3

AILPDLATQVLVPAAAVVIAFAVQWVLVSKVKMTAERRGEGSPGAAAGKDGGAASEY 62

Query: 62

LIEEEEGVNDQSVVAKCAEIQTaisegatsflfTEYKYXXXXXXXXXXXXXLSVEGF 121

LIEEEEG+N+ +VV KC+EIQ AISEGATSFLFTEYKY LGSVEGF

Sbjct: 63 LIEEEGLNEHNVVEKCSEIQAISEGATSFLFTEYKYVGLFMGIFAVLIFLFLGSVEGF

122

Query: 122

STDNKPCTYDTRRTCKPALATAAFSTIAFVLGAVTSVSGFLGMKIATYANARTTLEARK 181

ST ++PC Y R CKPALA A FST+AFVLGAVTS++SGFLGMKIATYANARTTLEARK

Sbjct: 123

STKSQPCHYSKDRMCKPALANAIFSTVAFVLGAVTSVSGFLGMKIATYANARTTLEARK 182

Query: 182

GVGKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSM 241

GVGKAFI AFRSGAVMGFLAASGL+VLYI IN+F IYYGDDWEGLFEAITGYGLGGSSM

Sbjct: 183

GVGKAFITAFRSGAVMGFLAASGLVVLYIAINLFGIYYGDDWEGLFEAITGYGLGGSSM 242

Query: 242

ALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAPIADNVGDNVGDIAGMGSDLFG 301

ALFGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAPIADNVGDNVGDIAGMGSDLFG

Sbjct: 243

ALFGRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAPIADNVGDNVGDIAGMGSDLFG 302

Query: 302 SYAEASCAA VVASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEI

361

SYAE+SCAALVVASISSFGINH+FT M YPLLISS+GI+ CLITTLFATDFFEIK V EI

Sbjct: 303 SYAESCAA VVASISSFGINHEFTPMLYPLLISSVGIIACLITTLFATDFFEIKAVDEI 362

Query: 362

EPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVKNWQLFLCVCVGLWAGLI 421

EPALK QLIISTV+MTVGIA+VSW+GLP SFTIFNFG QK V NWQLFLCV VGLWAGLI

Sbjct: 363

EPALKKQLIISTVWMTVGIALVSWLGLPYSFTIFNFGAQKTVYNWQLFLCVAVGLWAGLI 422

Query: 422

IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXX 481

IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 423 IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAFSIFLSFSLA
482

Query: 482

XMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTTA 541

MYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTTA

Sbjct: 483

AMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTTA 542

Query: 542

AIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPVIIGLLVGAMLPYWFSAMTMKSV 601

AIGKGFAIGSAALVSLALFGAFVSRA I TVDVLTPV IGL+VGAMLPYWFSAMTMKSV

Sbjct: 543

AIGKGFAIGSAALVSLALFGAFVSRAAISTVDVLTPVFIGLVGAMLPYWFSAMTMKSV 602

Query: 602

GSAALKMVEEVRRQFNTPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVG 661

GSAALKMVEEVRRQFN+IPGLMEGT KPDYATCVKISTDASIKEMIPPG LVML+PLIVG

Sbjct: 603

GSAALKMVEEVRRQFNIPGLMEGTTKPDYATCVKISTDASIKEMIPPGALVMLSPLIVG 662

Query: 662

FFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHK 721

FFGVETLSG+LAG+LVSGVQIAISASNTGGAWDNAKKYIEAG SEHA++LGPKGS+ HK

Sbjct: 663

IFFGVETLSGLLAGALVSGVQIAISASNTGGAWDNAKKYIEAGASEHARTLGPKGSDCHK 722

Query: 722 AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFK+F

Sbjct: 723 AAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKWF 771

>gi|31580801|gb|AAP55210.1| vacuolar proton-inorganic pyrophosphatase [Triticum aestivum]

Length = 762

Score = 1132 bits (2928), Expect = 0.0

Identities = 612/765 (80%), Positives = 664/765 (86%), Gaps = 5/765 (0%)

Query: 5 ALLPELWTEILVPICAVIGIAFSLFQWYVVSRVKLTSDLXXXXXXXXXXXXXXDYLIE

64

A+L EL TEIL+P+C V+GI F++ QW++VS+VK+T DYLIE

Sbjct: 2 AILGELGTEILIPVCVGVGIVFAVAQWFIVSKVKTPGAASAAGGGKNGYG---DYLIE 57

Query: 65

EEEGVNDQSVVAKCAEIQTASEGATSFLTEYKYXXXXXXXXXXXXXLSVGSVEGFSTD 124

EEEG+ND +VV KCAEIQTASEGATSFLFT Y+Y LGS+EGFST

Sbjct: 58

EEEGLNDHNVVVKCAEIQTASEGATSFLFTMYQYVGMFMVVFAAVIFVFLGSIEGFSTK 117

Query: 125

NKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGVG 184

+PCTY +T TCKPAL TA FST +F+LGA+TS++SGFLGMKIATYANARTTLEARKGVG

Sbjct: 118 GQPCTY-

STGTCKPALYTALFSTASFLLGAITSVSGFLGMKIATYANARTTLEARKGVG 176

Query: 185

KAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSMALF 244

KAFI AFRSGAVMGFL++SGL VLYITINVFK+YYGDDWEGLFE+ITGYGLGGSSMALF

Sbjct: 177

KAFITAFRSGAVMGFLSSSGLGVLYITINVFKMYYGDDWEGLFESITGYGLGGSSMALF 236

Query: 245

GRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYA 304
GRVGGGIYTKAADVGADLVGK+ERNIPED PRNPAVIADNVGDNVGDIAGMGSDLFGSYA

Sbjct: 237

GRVGGGIYTKAADVGADLVGKVERNIPEDGPRNPAVIADNVGDNVGDIAGMGSDLFGSYA 296

Query: 305 EASCAALVVASISSLFGINHDFTAMCYPLLSSMGILVCLITTLFATDFFEIKLVKEIEPA
364

E+SCAALVVASISSLFGINHDFTAMCYPLL+SS+GI+VCL+TTLFATDFFEIK EIEPA

Sbjct: 297 ESSCAALVVASISSLFGINHDFTAMCYPLLSSVGIVCLLTLFATDFFEIKAASEIEPA
356

Query: 365 LKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGLIIGF
424

LK QLII T +MT+G+A+++W+ LP FTIFNFG QK V NW LF CV VGLWAGLIIGF

Sbjct: 357 LKKQLIIFTALMTIGVAVINVWLPAKFTIFNFGAQKDVSNWGLFFCVAVGLWAGLIIGF
416

Query: 425

VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXMY 484
VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK MY

Sbjct: 417 VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSIIPIFAIAVSIYVSFSIAAMY
476

Query: 485

GVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTAAIG 544
G+A+AALGMLST ATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTAAIG

Sbjct: 477

GIAMAALGMLTTATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTAAIG 536

Query: 545

KGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKSVGSA 604

KGFAIGSAALVSLALFGAFVSrag+ VDVL+PKV IGL+VGAMLPYWFSAMT + SA

Sbjct: 537

KGFAIGSAALVSLALFGAFVSAGVKVVDSLSPKVFIGLIVGAMLPYWFSAMTRRVCESA 596

Query: 605

ALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFFF 664

ALKMVE+VRRQFNTIPGLM+GTAKPDYATCVKISTDASI+EMIPPG LVMLTPLIVG F

Sbjct: 597

ALKMVEKVRRQFNTIPGLMKGTAKPDYATCVKISTDASIREMIPPGALVMLTPLIVGTLF 656

Query: 665

GVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHKA AV 724

GVETLSGVLAG+LVSGVQIAISASNTGGAWDNAKKYIEAG SEHA+SLGPKGS+ HKA AV

Sbjct: 657

GVETLSGVLAGALVSGVQIAISASNTGGAWDNAKKYIEAGNSEHARSLGPKGSDCHKA AV 716

Query: 725 IGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKY 769

IGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFAT+GG+LFKY

Sbjct: 717 IGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATYGGVLFKY 761



>gi|7739779|gb|AAF69010.1| H+-pyrophosphatase [Vitis vinifera]

Length = 759

Score = 1109 bits (2868), Expect = 0.0

Identities = 601/765 (78%), Positives = 665/765 (86%), Gaps = 10/765 (1%)

Query: 5 ALLPELWTEILVPICAVIGIAFSLFQWYVVSRVKLTSDLXXXXXXXXXXXXDYIE
64

++ + +T++L+P+ A++GI F+L QW +VS+VK+++D D LIE

Sbjct: 2 GVMGDAFTQLLIPVAALVGIGFALLQWLLSKVKVSAD-----SDLNNNGYSDRLIE 52

Query: 65 EEE-

GVNDQS VVAKCAEI QTASEGATSFLFTEY KYXXXXXXXXXXXXXXLGSVEGFST 123

EEE G++ + V AKCAEIQ AIS GATSFLFTEY+Y LGSV+GFST

Sbjct: 53 EEEEGIDHEDVAAKCAEI QNAISVGATSFLFTEY RYLSIFMGVFGAIIFLFLGSVKGFST

112

Query: 124

DNKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGV 183
++PCTY+T CKPALA A FSTIAF+LGA+TSV SGFLGMKIATYANARTTLEARKGV

Sbjct: 113

KSEPCPTYNTGSLCKPALANALFSTIAFLGAMTSVSGFLGMKIATYANARTTLEARKGV 172

Query: 184

GKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFITAIGYGLGGSSMAL 243
GKAFIVAFRSGAVMGFLAASGLLVLY++I++F +YYGDDWEGL+E+ITGYGLGGSSMAL

Sbjct: 173

GKAFIVAFRSGAVMGFLAASGLLVLYVSIHLFSLYYGDDWEGLYESITGYGLGGSSMAL 232

Query: 244

FGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAPIADNVGDNVGDIAFMGSDFGSY 303

FGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAPIADNVGDNVGDIAFMGSDFGSY

Sbjct: 233

FGRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAPIADNVGDNVGDIAFMGSDFGSY 292

Query: 304 AEASCAALVVASISSFGINHDFTAMCYPLLISSMGLVCLITLFADEEIKLVKEIEP
363

AEASCAAL VASISSFGI+HD+TAM +PL+ISS+GI+VCL TTLFADEEIKLVKEIEP

Sbjct: 293 AEASCAALVVASISSFGISHDYTAMSFPILISSVGIVVCLGTTLFATDFVEIKNVSEIEP
352

Query: 364 ALKNQLIISTVIMTVGIAIVSWGLPTSFTIFNFGTQKVVKNWQLFLCVGLWAGLIIG
423

+LK QL+IST++MT GIA+VS+ LP+ FT+FNFG+ K VKNW LF CV +GLWAGL+IG

Sbjct: 353 SLKRQLLISTILMTAGIAVVSFFALPSEFTLFNFGSTKTVKNWHLFFCVSIGLWAGLVIG
412

Query: 424

FVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXX 483
++TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK M

Sbjct: 413 YITEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAIAIYVSFSMAAM
472

Query: 484

YGAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTAAI 543
YG+AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSH+IR+RTDALDAAGNTAAI

Sbjct: 473

YGIAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHKIRQRTDALDAAGNTAAI 532

Query: 544

GKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKSVGS 603
GKGFAIGSAALVSLALFGAFVSRAGI TVDVLTPKV IGL+VGAMLPYWFSAMTMKSVGS

Sbjct: 533

GKGFAIGSAALVSLALFGAFVSRAGIETVDVLTPKFIGLIVGAMLPYWFSAMTMKSVGS 592

Query: 604

AALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFF 663
AALKMVEEVRRQFNTIPGLMEG AKPDYATCVKISTDAS++EMIPPG LVMLTPLI G

Sbjct: 593

AALKMVEEVRRQFNTIPGLMEGRAKPDYATCVKISTDASLREMIPPGALVMLTPLIAGTL 652

Query: 664

FGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHKAA 723
FGVETL+GVLAGSLVSGVQ+AISASNTGGAWDNAKKYIEAG SEHA+SLGPKGS+PHKAA

Sbjct: 653

FGVETLAGVLAGSLVSGVQVAISASNTGGAWDNAKKYIEAGASEHARSLGPKGSDPHKAA 712

Query: 724 VIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFK 768

VIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFA HGG+LFK

Sbjct: 713 VIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFAHGGLLFK 757

- gi|7436042|pir|S72527 inorganic diphosphatase (EC 3.6.1.1), H⁺-translocating, vacuolar membrane (clone OVP2) - rice
- gi|1747296|dbj|BAA08233.1| vacuolar H⁺-pyrophosphatase [Oryza sativa (japonica cultivar-group)]
- gi|3298476|dbj|BAA31524.1| ovp2 [Oryza sativa]
- gi|24413986|dbj|BAC22237.1| putative inorganic pyrophosphatase [Oryza sativa (japonica

cultivar-group)]

Length = 767

Score = 1146 bits (2964), Expect = 0.0

Identities = 618/766 (80%), Positives = 667/766 (87%)

Query: 5 ALLPELWTEILVPICAVIGIAFSLFQWYVVSRVKLTSDLXXXXXXXXXXXXXXDYLIE
64

A+L L TE+ +P+ A +G+AF++ QW +V+RVK+ DYLIE

Sbjct: 2

AILSALGTEVFIPVAAAVGVAFAVAQWLLVARVKVNPAHAAAAASGGSKNGGYGDYLIE 61

Query: 65

EEEGVNDQSVAKCAEIQTaisegatsflfteykyxxxxxxxxxxxxxxlgsvegfstd 124

EEEG+ND +VV KC EIQTaisegatsflftey+y lgsvegfst

Sbjct: 62 EEEGLNDHNWVKCHEIQTaisegatsflfteyqyvgifmsifavviflflgsvegfstk
121

Query: 125

NKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGVG 184
++PCTY + CKPAL A FST +F+LGA+TS++SG+LGMKIAT+ANARTTLEARKGVG

Sbjct: 122

SQPCTYSKDKYCKPALFNALFSTASFLGAITSVSGYLGMIATFANARTTLEARKGVG 181

Query: 185

KAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEITGYGLGGSSMALF 244
KAFI+AFRSGAVMGFLA+SGL+VLYI INVFK+YYGDDWEGLFE+ITGYGLGGSSMALF

Sbjct: 182

KAFIIAFRSGAVMGFLASSGLVVLVYIAINVFKLYYGDDWEGLFESITGYGLGGSSMALF 241

Query: 245

GRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAPIADNVGDNVGDIAFMGSDFGSYA 304

GRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAPIADNVGDNVGDIAFMGSDFGSYA

Sbjct: 242

GRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAPIADNVGDNVGDIAFMGSDFGSYA 301

Query: 305 EASCAALVVASISSFGINHDFTAMCYPLLISSMGLVCLITTLFATDFFEIKLVKEIEPA
364

E+SCAALVVASISSFGINHDFT MCYPLL+SS+GI+VCLITTLFATDFFEIK VKEIEPA

Sbjct: 302 ESSCAALVVASISSFGINHDFTGMCYPLLVSSVGIIVCLITTLFATDFFEIKAVKEIEPA
361

Query: 365 LKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVVGLWAGLIIGF
424

LK QLIIST +MTVGIAI+SW+ LP FTIFNFG QK V NW LF CV +GLWAGLIIGF

Sbjct: 362 LKKQLIISTALMTVGIAISWLALPAKFTIFNFGAQKEVTNWGLFFCVAIGLWAGLIIGF
421

Query: 425

VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXMY 484
VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK MY

Sbjct: 422 VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSIIPIFAIASIYVSFSIAAMY
481

Query: 485

GVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTAAIG 544
G+AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTAAIG

Sbjct: 482

GIAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTAAIG 541

Query: 545

KGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKSVGSA 604
KGFAIGSAALVSLALFGAFVSRA+ VDVL+PKV IGL+VGAMLPYWFSAMTMKSVGSA

Sbjct: 542

KGFAIGSAALVSLALFGAFVSRAVKVVDSLSPKVFIGLIVGAMLPYWFSAMTMKSVGSA 601

Query: 605

ALKMVEEVRRQFNTPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFFF 664

ALKMVEEVRRQFN+IPGLMEGT KPDYATCVKISTDASIKEMIPPG LVMLTPLIVG F

Sbjct: 602

ALKMVEEVRRQFNNSIPGLMEGTGKPDYATCVKISTDASIKEMIPPGALVMLTPLIVGTLF 661

Query: 665

GVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHKAAV 724

 GVETLSGVLAG+LVSGVQIAISASNTGGAWDNAKKYIEAG SEHA++LGPKGS+ HKAAV

Sbjct: 662

GVETLSGVLAGALVSGVQIAISASNTGGAWDNAKKYIEAGASEHARTLGPKGSDCHKAAV 721

Query: 725 IGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

 IGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGG+LFK+F

Sbjct: 722 IGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGLLFKF 767

□ >gi|30027157|gb|AAP06752.1| vacuolar proton-inorganic pyrophosphatase [Hordeum
brevisubulatum]

Length = 773

Score = 1166 bits (3016), Expect = 0.0

Identities = 634/772 (82%), Positives = 676/772 (87%), Gaps = 2/772 (0%)

Query: 1 MVAPALLPELWTEILVPICAVIGIAFSLFWYVVSRVKLTSD--LXXXXXXXXXXXXXX
58

 +VA A+LPEL T+++VP+ A +GIAF++ QW++VS+VK+ +

Sbjct: 2

VVAAAILPELATQLVVPVAAAVGIAFAVLQWFLVSKVKVAPERRGEGSAGAGGGKDGA 61

Query: 59

XDYLIEEEEGVNDQSVVAKCAEIQTaisegatsflteykyXXXXXXXXXXXXLGSV 118

 +YLIEEEEG+ND +VV KCAEIQTaisegatsflteyky LGS+

Sbjct: 62 SEYLIEEEGLNDHNVLKCAEIQTaisegatsflteykyAGGFMTVFAVLIFVFLGSI

121

Query: 119

EGFSTDNKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLE 178

 EGFST ++PC Y +TCKPALA AAFSTIAFVLGAVTS++SGFLGMKIATYANARTTLE

Sbjct: 122

EGFSTKSQPCHYSVGKTCKPALANA AFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLE 181

Query: 179

ARKGVGKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGG 238

ARKGVGKAFIVAFRSGAVMGFLAASGL VLY+ IN+F +YYGDDWEGLFEAITGYGLGG

Sbjct: 182

ARKGVGKAFIVAFRSGAVMGFLAASGLFVLYVAINLFGLYYGDDWEGLFEAITGYGLGG 241

Query: 239

SSMALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSD 298

SSMALFGRVGGGIYTK ADVGADLVGK ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSD

Sbjct: 242

SSMALFGRVGGGIYTKTADVGADLVGKEERNIPEDDPRNPAVIADNVGDNVGDIAGMGSD 301

Query: 299 LFGSYAEASCAALVVASISSFGINHDFTAMCYPLLISSMGLVCLITLFATDFFEIKLV
358

LFGSYAE+SCAALVVASISSFGINH+FT M YPLLISS+GI+ CLITLFATDFFE+K V

Sbjct: 302 LFGSYAEASSCAALVVASISSFGINHEFTPMMYPLLISSVGIACLITLFATDFFEIKEV
361

Query: 359

KEIEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVVGLWA 418

+IEPALK QLIIST +MTVGIA+VSW+GLP +FTIFNFG QK V +WQLFLCV VGLWA

Sbjct: 362

DQIEPALKKQLIISTAVMTVIALVSWLGLPYTFTIFNFGAQKTVHSWQLFLCVAVGLWA 421

Query: 419

GLIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXX 478

GL+IGF+TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 422 GLVIGFITEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAFSIFLSF
481

Query: 479

XXXXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGN 538

MYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGN

Sbjct: 482

SLAAMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGN 541

Query: 539

TTAAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTM 598

TTAAIGKGFAIGSAALVSLALFGAFVSRAGI TVDVLT P V IGLLVGAMLPYWFSAMTM

Sbjct: 542

TTAAIGKGFAIGSAALVSLALFGAFVSRAGITV DVLT PNVFIGLLVGAMLPYWFSAMTM 601

Query: 599

KSVGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIIPPGCLVMLTPL 658

KSVGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDAS KEMIPPG LVMTPL

Sbjct: 602

KSVGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASTKEMIPPGALVMLTPL 661

Query: 659

IVGFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSE 718

IVG FFGVETLSGVLAG+LVSGVQIAISASNTGGAWDNAKKYIEAG SEHAKSLGPKGS+

Sbjct: 662

IVGTFFGVETLSGVLAGALVSGVQIAISASNTGGAWDNAKKYIEAGASEHAKSLGPKGSD 721

Query: 719 PHKAAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

HKA AVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFAT+GGILFKY

Sbjct: 722 CHKAAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATYGGILFKYL 773



>gi|18086404|gb|AAL57660.1| At1g15690/F7H2_3 [Arabidopsis thaliana]

Length = 770

Score = 1315 bits (3402), Expect = 0.0

Identities = 717/770 (93%), Positives = 718/770 (93%)

Query: 1

MVAPALLPELWTEILVPICAVIGIAFSLFQWYVVSRVKLTSDLXXXXXXXXXXXXXXD 60

MVAPALLPELWTEILVPICAVIGIAFSLFQWYVVSRVKLTSDL D

Sbjct: 1

MVAPALLPELWTEILVPICAVIGIAFSLFQWYVVSRVKLTSDLGASSSGGANNGKNGYGD 60

Query: 61

YLIEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXLSVEG 120

YLIEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKY LGSVEG

Sbjct: 61 YLIEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYVGVMIFFAAVIFVFLGSVEG
120

Query: 121

FSTDNKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTLEAR 180

FSTDNKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTLEAR

Sbjct: 121

FSTDNKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTLEAR 180

Query: 181

KGVGKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS 240

KGVGKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS

Sbjct: 181

KGVGKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS 240

Query: 241

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDF 300

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDF

Sbjct: 241

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDF 300

Query: 301 GSYAEASCAAJVVASISSFGINHDFTAMCYPLLISSMGILVCLITLFATDFFIEIKLVKE
360

GSYAEASCAAJVVASISSFGINHDFTAMCYPLLISSMGILVCLITLFATDFFIEIKLVKE

Sbjct: 301 GSYAEASCAAJVVASISSFGINHDFTAMCYPLLISSMGILVCLITLFATDFFIEIKLVKE
360

Query: 361

IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGL 420

IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGL

Sbjct: 361 IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGL
420

Query: 421

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXX 480
IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGY

Sbjct: 421 IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAISIFVSFSF
480

Query: 481

XXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTT 540
MYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTT

Sbjct: 481
AAMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTT 540

Query: 541

AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKS 600
AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKS

Sbjct: 541
AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKS 600

Query: 601

VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV 660
VGSAALKMVEEVRRQFNTIPGLM+GTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV

Sbjct: 601
VGSAALKMVEEVRRQFNTIPGLMKGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV 660

Query: 661

GFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYEAGVSEHAKSLGPKGSEPH 720
GFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYEAGVSEHAKSLGPKGSEPH

Sbjct: 661
GFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYEAGVSEHAKSLGPKGSEPH 720

Query: 721 KAAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

KAAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF
Sbjct: 721 KAAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

>gi|542059|pir|S42893 inorganic diphosphatase (EC 3.6.1.1) - common tobacco
gi|457744|emb|CAA54869.1| inorganic pyrophosphatase [Nicotiana tabacum]
Length = 764

Score = 1197 bits (3096), Expect = 0.0

Identities = 644/769 (83%), Positives = 682/769 (88%), Gaps = 5/769 (0%)

Query: 2 VAPALLPELWTEILVPICAVIGIAFSLFQWYVSRVKLTSDLXXXXXXXXXXXXXXDY

61

+ ALLP+L T+I++P+CAVIGI FS FQWY+VSrvK++S+ D

Sbjct: 1

MGSALLPDGTQIVIPVCAVIGIVFSSFWYLVSrvKVSSEHGATSPSSNKNNKNGYGDC 60

Query: 62

LIEEEEGVNDQSVVAKCAEIQTaiseGATsFLFTEYKYXXXXXXXXXXXXXLSVEGF 121

LIEEEEG+ND +VVAKCA+IQ AISEGATsFLFTEY+Y LGSVEGF

Sbjct: 61 LIEEEEGINDHNVVAKCADIQNAISEGATsFLFTEYQYVGIFMIAFAILIFLFLGSVEGF

120

Query: 122

STDNKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARK 181

ST ++PCTY+ + CKPALATA FST++F+LGA+TSV+SGFLGMKIATYANARTTLEARK

Sbjct: 121 STSSQPCTYNKEKRCKPALATAIFSTVSFLGAITSVISGFLGMKIATYANARTTLEARK

180

Query: 182

GVGKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSM 241

GVGKA +V VMGFLAA+GLLVLYI IN+FK+YYGDDWEGLFEAITGYGLGGSSM

Sbjct: 181 GVGKACLVQ----VMGFLAANGLLVLYIAINLFKLYYGDWEGLFEAITGYGLGGSSM

235

Query: 242

ALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAPIADNVGDNVGDIAFMGSDLFG 301

ALFGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAPIADNVGDNVGDIAFMGSDLFG

Sbjct: 236

ALFGRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAPIADNVGDNVGDIAFMGSDLFG 295

Query: 302 SYAEASCAALVVASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEI
361

SYAE+SCAALVVASISSFGI+HDFTAMCYPLLISSMGILVCLITTLFATDFFEIK VKEI

Sbjct: 296 SYAESSCAALVVASISSFGIDHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKAVKEI
355

Query: 362

EPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGLI 421

EPALKNQLIIST IMTVGIAIV+W LP+SFTIFNFGTQKVVKNWQLFLCV VGLWAGLI

Sbjct: 356 EPALKNQLIISTAINTVGGIAIVTWTCPLSSFTIFNFGTQKVVKNWQLFLCVAVGLWAGLI
415

Query: 422

IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXX 481

IGFVTEYYTSNAYSPVQDVADSC TGAATNVIFGLALGYK

Sbjct: 416 IGFVTEYYTSNAYSPVQDVADSCSTGAATNVIFGLALGYKSVIPIFAIAIAIFVSFTFA
475

Query: 482

XMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTTA 541

MYG+AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTTA

Sbjct: 476

AMYGIAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTTA 535

Query: 542

AIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPVIIGLLVGAMLPYWFSAMTMKSV 601

AIGKGFAIGSAALVSLALFGAFVSRAFI TVDVLTP+V IGL+VGAMLPYWFSAMTMKSV

Sbjct: 536

AIGKGFAIGSAALVSLALFGAFVSRAFISTVDVLTPQVFIGLIVGAMLPYWFSAMTMKSV 595

Query: 602

GSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVG 661

GSAALKMVEEVRRQFNTIPGLMEG AKPDYATCVKISTDASIKEMIPPG LVMLTPLIVG

Sbjct: 596

GSAALKMVEEVRRQFNTIPGLMEGLAKPDYATCVKISTDASIKEMIPPGALVMLTPLIVG 655

Query: 662

FFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHK 721

FFGVETLSGVLAG+LVSGVQIAISASNTGGAWDNAKKYIEAG SEHA++LGPKGSEPHK

Sbjct: 656

IIFGVETLSGVLAGALVSGVQIAISASNTGGAWDNAKKYIEAGASEHARTLGPKGSEPHK 715

Query: 722 AAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

AAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFK F

Sbjct: 716 AAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKIF 764

>gi|25901033|dbj|BAC41250.1| vacuolar proton-inorganic pyrophosphatase [Pyrus
communis]

Length = 767

Score = 1188 bits (3073), Expect = 0.0

Identities = 643/765 (84%), Positives = 681/765 (89%), Gaps = 1/765 (0%)

Query: 6 LLPELWTEILVPICAVIGIAFSLFQWYVSRVKLTSDLXXXXXXXXXXXXXXDYLIEE
65

LL L TEI++P+ AV+GI FSL QW++VS VK+T + DYLIEE

Sbjct: 4 LLSTLATEIVIPVAAVGIVFSLVQWFLVSLVKVTPE-RNAPPSPNSNKNGCNDYLIEE
62

Query: 66

EEGVNDQSVVAKCAEIQTAISEGATSLFTYEKYXXXXXXXXXXXXXLSVEGFSTDN 125

EEG+NDQ+VV KCAEIQ AISEG+TSFLFT Y+Y LGSVEGFST +

Sbjct: 63

EEGLNDQNVVKCAEIQN AISEGSTSFLFTMYQYVGFMVVFAILIFLFLGSVEGFSTKS 122

Query: 126

KPCTYDTRRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGVGK 185

+PCTYD +TCKPALATA FST+AFVLG +TSVLSGFLGMKIATYANARTTLEARKGVGK

Sbjct: 123

QPCTYDAAKTCKPALATAIFSTVAFVLGGITSVLSGFLGMKIATYANARTTLEARKGVGK 182

Query: 186

AFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSMALFG 245

AFI AFRSGAVMGFLAA+GLLVL+ITIN+FK+YYGDDWEGLFE+ITGYGLGGSSMALFG

Sbjct: 183

AFITAFRSGAVMGFLAANGLLVLFITINLFKLYYGDDWEGLFESITGYGLGGSSMALFG 242

Query: 246

RVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAE 305

RVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAE

Sbjct: 243

RVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAE 302

Query: 306 ASCAALVVASISSLFGINHDFTAMCYPLLISSMGLVCLITTLFATDFFEIKLVKEIEPAL
365

+SCAALVVASISSLFGINH+FT M YPLLISS+GI+VCLITTLFATDFFEIK VKEIEPAL

Sbjct: 303 SSCAALVVASISSLFGINHEFTPMLYPLLISSVGIVCLITTLFATDFFEIKAVKEIEPAL 362

Query: 366 KNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCGWLWAGLIIGFV
425

K QLIISTV+MT+GIAIVSW+ LP+SFTIFNFG QKVVKNWQLFLCV VGLWAGLIIGFV

Sbjct: 363 KKQLIISTVLMТИGIAIVSWIALPSSFTIFNFGVQKVVKNWQLFLCVAVGLWAGLIIGFV
422

Query: 426

TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXMYG 485

TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK MYG

Sbjct: 423 TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSIIPIFAIAVSIYVSFSFAAMYG
482

Query: 486

VAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTAAIGK 545

+AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTAAIGK

Sbjct: 483

IAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTAAIGK 542

Query: 546

GFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKSVGSAA 605

GFAIGSAALVSLALFGAFVSRA I TVDVLTPKV IGL+VGAMLPYWFSAMTMKSVGSAA

Sbjct: 543

GFAIGSAALVSLALFGAFVSRAAISTDVLTpvfigLIVGAMLPYWFSAMTMKSVGSAA 602

Query: 606

LKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFFFG 665

LKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPG LV+LTPLIVG FFG

Sbjct: 603 LKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGALVLTPLIVGTF

662

Query: 666

VETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHKAAVI 725

VETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAG SEHA++LGPKGS+PHKAAVI

Sbjct: 663

VETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGASEHARTLGPKGSDPHKAAVI 722

Query: 726 GDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

GDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGG+LFK F

Sbjct: 723 GDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGLLFKIF 767



>gi|22532391|gb|AAM97920.1| vacuolar proton-pumping PPase [Chenopodium rubrum]

gi|22532393|gb|AAM97921.1| vacuolar proton-pumping PPase [Chenopodium rubrum]

Length = 764

Score = 117.9 bits (3049), Expect = 0.0

Identities = 638/765 (83%), Positives = 678/765 (88%), Gaps = 5/765 (0%)

Query: 6 LLPELWTEILVPICAVIGIAFSLFQWYVVSRVKLTSDLXXXXXXXXXXXXXXDYLIEE

65

LLP+L TEIL+P+CAVIGI FSL QWYVVS+VKL+ D + LIEE

Sbjct: 5 LLPDLGTEILIPVCAVIGIVFSLIQWYVVSVVKLSPD----SGRSNNNKNGFSENLIEE 59

Query: 66

EEGVNDQSVVAKCAEIQTaisegatsflfTEYKYXXXXXXXXXXXXXXLGSVEGFSTDN 125

EEG+NDQSVVAKCAEIQ AISEG+TSFL+T Y+Y LGSVEGFST +

Sbjct: 60 EEGINDQSVVAKCAEIQNaisegstsflytmyqyvgifmiafavlifvflgsvegfstks
119

Query: 126

KPCTYDTRRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGVGK 185

+ CTYD ++TCKPALATA FST++F+LGAVTS+ SGFLGMKIATYANARTTLEARKGVGK

Sbjct: 120

QECTYDKSKTCKPALATAIFSTSFLGAVTLSASGFLGMKIATYANARTTLEARKGVGK 179

Query: 186

AFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSMALFG 245

AFIVAFRSGAVMGFLAA+GLLVLYITI +FK+YYGDDWEGLFEAITGYGLGGSSMALFG

Sbjct: 180

AFIVAFRSGAVMGFLLAANGLLVLYITILLFKLYYGDDWEGLFEAITGYGLGGSSMALFG 239

Query: 246

RVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAPIADNVGDNVGDIAGMGSDFGSYAE 305

RVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAPIADNVGDNVGDIAGMGSDFGSYAE

Sbjct: 240

RVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAPIADNVGDNVGDIAGMGSDFGSYAE 299

Query: 306 ASCAALVVASIISSEGINHDFTAMCYPLLISSMGILVCLITLFATDFFIEKLVKEIEPAL
365

+SCAALVVASIISSEGINH+ TA+ YPLLISS+GI++CLITLFATDFFIEIK VKEIEPAL

Sbjct: 300 SSAACALVVASIISSEGINHELTAILYPLLISSVGIVICLITLFATDFFIEIKAVKEIEPAL 359

Query: 366 KNQLIISTVIMTVGIAIVSWGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGLIIGFV
425

K QL+IST +MTV +A++SWV LP+SFTIF+FG+Q+ VKNWQLFLCV VGLWAGLIIGFV

Sbjct: 360

KKQLVISTALMTVAVAVISWVALPSSFTIFDFGSQREVKNWQLFLCVAVGLWAGLIIGFV 419

Query: 426

TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXMYG 485

TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

MYG

Sbjct: 420 TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAVSIFVSFSFAAMYG
479

Query: 486

VAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTAAIGK 545
+AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTAAIGK

Sbjct: 480

IAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTAAIGK 539

Query: 546

GFAIGSAALVSLALFGAFVSRAI TVDVLTPV IGLLVGAMLPYWFSAMTMKSVGSAA 605
GFAIGSAALVSLALFGAFVSRAI TVDVLTPV IGLLVGAMLPYWFSAMTMKSVGSAA

Sbjct: 540

GFAIGSAALVSLALFGAFVSRAAISTVDVLTPVFIGLLVGAMLPYWFSAMTMKSVGSAA 599

Query: 606

LKMVEEVRRQFNIPGLMEGTAKPDYATCVKISTDASIKEIMPAGCLVMLTPLIVGFFF 665
LKMVEEVRRQFN IPGLMEGTAKPDY CVKISTDASIKEIMPAG LVMLTPLIVG FG

Sbjct: 600

LKMVEEVRRQFNEIPGLMEGTAKPDYANCVKISTDASIKEIMPAGALVMLTPLIVGTLFG 659

Query: 666

VETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHKAAVI 725
VETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAG SEHA+ LGPKGS+ HKAAVI

Sbjct: 660

VETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGASEHARQLGPKGSDAHKAAVI 719

Query: 726 GDTIGDPLKDTGPSLNILIKLMAVESL VFAPFFATHGGILFKYF 770

GDTIGDPLKDTGPSLNILIKLMAVESL VFAPFFATHGG+LFK F

Sbjct: 720 GDTIGDPLKDTGPSLNILIKLMAVESL VFAPFFATHGGLLFKIF 764

>gi|7436047|pir||T14564 inorganic diphosphatase (EC 3.6.1.1), vacuolar- beet
gi|485744|gb|AAA61610.1| pyrophosphatase [Beta vulgaris]

Length = 765

Score = 1168 bits (3022), Expect = 0.0

Identities = 635/770 (82%), Positives = 677/770 (87%), Gaps = 6/770 (0%)

Query: 2 VAPALLPELWTEILVPICAVIGIAFSLFQWYVVSRVKLTSDLXXXXXXXXXXXXXXDY
61

+ ALLP+L TEI++P+CAVIGIAFSL QWY+V RVKL+ D D

Sbjct: 1 MGAALLPDLITEIIIPVCAVIGIAFSLLQWYIVLRVKLSPD----STRNNNNKNGFSDS 55

Query: 62

LIEEEEGVNDQSVVAKCAEIQTaisegatsflfteykyxxxxxxxxxxxxxlgsvgef 121

LIEEEEG+NDQSVVAKCAEIQ AISEGATSFLFTEY+Y LGSVEGF

Sbjct: 56 LIEEEGLNDQSVVAKCAEIQNaisegatsflfteyqyvgifmvaflvlflgsvegf
115

Query: 122

STDNKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARK 181

ST ++ CTYD TR CKPALATA FST+AF+LGA+TS+ SGF GMKIATYANARTTLEARK

Sbjct: 116

STSSQECTYDKTRRCKPALATAIFSTVAFLLAGITSLGSGFFGMKIATYANARTTLEARK 175

Query: 182

GVGKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSM 241

GVGKAFIVAFRSGAVMGFLAA+GLLVLYITI +FKIYYGDDWEGLFEAITGYGLGGSSM

Sbjct: 176

GVGKAFIVAFRSGAVMGFLAANGLLVLYITILLFKIYYGDDWEGLFEAITGYGLGGSSM 235

Query: 242

ALFGRVGGGIYTKAADVGADELVGKIERNIPEDDPRNPAVIADNVGDNVGDAGMGSDF- 300

ALFGRV GGIYTKAADVGADELVGK+ER+IPEDDPRNPAVIADNVGDNVGDAG G +F

Sbjct: 236

ALFGRVAGGIYTKAADVGADELVGKVERDIPEDDPRNPAVIADNVGDNVGDAGYGVLIFL 295

Query: 301 GSAYEASCAAJVVASISSFGINHDFTAMCYPLLISSMGLVCLITLFATDFFEIKLVKE
360

SYAE+SCAALVV SISSFGI+HD TAM YPLL+SS+GI+VCLITLFATDFFEIK VKE

Sbjct: 296 DSYAESSCAALVVRSISSFGISHDLTAMMYPLLVSSVGIVCLITLFATDFFEIKAVKE
355

Query: 361

IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVKWNWQLFLCVCVGLWAGL 420

IEPALK QLIIST +MTVG+A++SW+ LPTSFTIF+FG+QK V+NWQLFLCV VGLWAGL

Sbjct: 356 IEPALKKQLIISTALMTGVAVISWIALPTSFTIFDFGSQKEVQNWLQLFCAVGLWAGL
415

Query: 421

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXX 480

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 416 IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAISIFVSFSF
475

Query: 481

XXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTT 540

MYG+A+AALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTT

Sbjct: 476

AAMYGIAMAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTT 535

Query: 541

AAIGKGFAIGSAALVSLALFGAFVSRA | TVDVLPKV IGL+VGAMLPYWFSAMTMKS 600

AAIGKGFAIGSAALVSLALFGAFVSRA | TVDVLPKV IGL+VGAMLPYWFSAMTMKS

Sbjct: 536

AAIGKGFAIGSAALVSLALFGAFVSRA | TVDVLPKV IGL+VGAMLPYWFSAMTMKS 595

Query: 601

VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV 660

VGSAALKMVEEV +QFNTIPGL+EGTAKPDYATCVKISTDASIKEMIPPG LVMLTPLIV

Sbjct: 596 VGSAALKMVEEVPKQFNTIPGLLEGTAKPDYATCVKISTDASIKEMIPPGALVMLTPLIV
655

Query: 661

GFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPH 720

G FFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAG SEHA++LGPKGS+ H

Sbjct: 656

GTFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGASEHARTLGPKGSDAH 715

Query: 721 KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGG+LFKY

Sbjct: 716 KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGLLFKYL 765

□ >gi|11527561|dbj|BAB18681.1| vacuolar proton-inorganic pyrophosphatase [Hordeum vulgare subsp. vulgare]
Length = 771

Score = 1157 bits (2994), Expect = 0.0

Identities = 632/769 (82%), Positives = 674/769 (87%), Gaps = 1/769 (0%)

Query: 1 MVAPALLPELWTEILVPICAVIGIAFSLFQWYVSRVKLTSD-LXXXXXXXXXXXXXX
59

MVA A+LPEL T+++VP+ A +GIAF++ QW +VS+VK+ +

Sbjct: 1

MVAAAILPELATQLVVPVAAAVGIAFAVLQWVLVSKVKVAPEPRAEGGSASAVGAKDGAT 60

Query: 60

DYLIEEEEGVNNDQSVVAKCAEIQTaisegatsflfTEYKYXXXXXXXXXXXXXLSVE 119

+YLIIEEEEG+ND +VV KCAEIQTaiseg TSFLFTEYKY LGS+E

Sbjct: 61 EYLIEEEGLNDHNVLKCAEIQTaisegqtsflfTEYKYAGGFMTIFAVLIFVFLGSIE

120

Query: 120

GFSTDNKPCYYDTTRTCKPALATAAFSTIAFVLGAVTSVSGFLGMKIATYANARTTLEA 179

GFST ++PC Y +TCKPALA AAFSTIAFVLGAVTS++SGFLGMKIATYANARTTLEA

Sbjct: 121

GFSTKSQPCHYSVGKTCKPALANAAFSTIAFVLGAVTSVSGFLGMKIATYANARTTLEA 180

Query: 180

RKGVGKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGS 239

RKGVGKAFI AFRSGAVMGFLAASGL VLY+ IN+F +YYGDDWEGLFEAITGYGLGGS

Sbjct: 181

RKGVGKAFITAFRSGAVMGFLAASGLFVLYVAINLFGLYYGDDWEGLFEAITGYGLGGS 240

Query: 240

SMALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDAGMGSSDL 299

SMALFGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDAGMGSSDL

Sbjct: 241

SMALFGRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDAGMGSSDL 300

Query: 300 FGSYAEASCAALVVASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVK

359

FGSYAE+SCAALVVASISSFGINH+FT M YPLLISS+GI+ CLITTLFATDFFE+K V

Sbjct: 301 FGSYAESSCAALVVASISSFGINHEFTPMMYPLLISSVGIACLITTLFATDFFEVEVKEVD

360

Query: 360

EIEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVKNWQLFLCVVGLWAG 419

+IEPAL K QLIIST +MT+GIA+VSW+GLP +FTIFNFG QK V +WQLFLCV VGLWAG

Sbjct: 361

QIEPALKRQLIISTAVMTIGIALVSWLGLPYTFTIFNFGAQKTVHSWQLFLCVAVGLWAG 420

Query: 420

LIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXX 479

L+IGF+TEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 421 LVIGFITEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAFSIFLSFS

480

Query: 480

XXXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNT 539

MYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNT

Sbjct: 481

LAAMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNT 540

Query: 540

TAAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMK 599

TAAIGKGFAIGSAALVSLALFGAFVSRAGI TVDVLTP V IGLLVGAMLPYWFSAMTMK

Sbjct: 541

TAAIGKGFAIGSAALVSLALFGAFVSRAGITTVDVLTPNFIGLLVGAMLPYWFSAMTMK 600

Query: 600

SVGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLI 659

SVGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPG LVMLTPLI

Sbjct: 601

SVGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGALVMLTPLI 660

Query: 660

VGFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEP 719

VG FGVETLSGVLAG+LVSGVQIAISASNTGGAWDNAKKYIEAG SEHAKSLGPKGS+

Sbjct: 661

VGTLFGVETLSGVLAGALVSGVQIAISASNTGGAWDNAKKYIEAGASEHAKSLGPKGSDC 720

Query: 720 HKAAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFK 768

HKAAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFAT+GGILFK

Sbjct: 721 HKAAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATYGGILFK 769



>gi|3402487|dbj|BAA32210.1| Vacuolar proton pyrophosphatase [Arabidopsis thaliana]

Length = 770

Score = 1311 bits (3392), Expect = 0.0

Identities = 717/770 (93%), Positives = 717/770 (93%)

Query: 1

MVAPALLPELWTEILVPICAVIGIAFSLFWYVVSRVKLTSDLXXXXXXXXXXXXXXD 60

MVAPALL ELWTEILVPICAVIGIAFSLFWYVVSRVKLTSDL D

Sbjct: 1

MVAPALLLELWTEILVPICAVIGIAFSLFWYVVSRVKLTSDLGASSSGGANNGKNGYGD 60

Query: 61

YLIEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXLSVEG 120

YLIEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKY LGSVEG

Sbjct: 61 YLIEEEGVNDQSVVAKCAEIQTASEGATSFLFTEYKYVGFMIFAAVIFVFLGSVEG

120

Query: 121

FSTDNKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTLEAR 180

FSTDNKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTLEAR

Sbjct: 121

FSTDNKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTLEAR 180

Query: 181

KGVGKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS 240

KGVGKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS

Sbjct: 181

KGVGKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS 240

Query: 241

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDF 300

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDF

Sbjct: 241

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDF 300

Query: 301 GSYAEASCAALVVASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFIEIKLVKE

360

GSYAEASCAALVVASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFIEIKLVKE

Sbjct: 301 GSYAEASCAALVVASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFIEIKLVKE

360

Query: 361

IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGL 420

IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGL

Sbjct: 361 IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGL

420

Query: 421

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXX 480

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 421 IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIIPFAIAISIFVSFSF

480

Query: 481

XXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT 540

MYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT

Sbjct: 481

AAMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT 540

Query: 541

AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKS 600

AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKS

Sbjct: 541

AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKS 600

Query: 601

VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV 660

VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV

Sbjct: 601

VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV 660

Query: 661

GFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYEAGVSEHAKSLGPKGSEPH 720

GFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYEAGVSEHAKSLGPKGSEPH

Sbjct: 661

GFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYEAGVSEHAKSLGPKGSEPH 720

Query: 721 KAAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

KAAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF

Sbjct: 721 KAAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

>gi|45479863|gb|AAS66771.1| PPase [Hevea brasiliensis]
Length = 769

Score = 1207 bits (3122), Expect = 0.0

Identities = 651/766 (84%), Positives = 685/766 (89%)

Query: 5 ALLPELWTEILVPICAVIGIAFSLFWYVVSRVKLTSDLXXXXXXXXXXXXXXDYLIE

64

A+L EL TEILVP+CAV+GI FSL QWY+VSrvkLT + D LIE

Sbjct: 4 AVLSELGTEILVPVCAVGIVFSLIQWYLVSrvkLT PERQAPGSSPAGANKNGYNDCLIE
63

Query: 65

EEEGVNDQSVVAKCAEIQTaisegatsflfTEYKYXXXXXXXXXXXXXLSVegfstd 124

EEEG+ND SVVAKCAEI+TAISEGATSF LFTEY+Y LGSVEGFST

Sbjct: 64 EEEGLNDHSVVAKCAEIRTAISEGATSF LFTEYQYVGVMVAFAILIFLFLGSVEGFSTK
123

Query: 125

NKPCTYDTTRTCKPALATAAFSTIAVLGAVTSVLSGFLGMKIATYANARTTLEARKGVG 184

++PCTYD +TCKPALATA FST++F+LGA TSV+SGFLGMKIATYANARTTLEARKGVG

Sbjct: 124

SQPCTYDKQKTCKPALATAIFSTVSFLLGAFTSVSGFLGMKIATYANARTTLEARKGVG 183

Query: 185

KAFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEITGYGLGGSSMALF 244

KAFI AFRSGAVMGFLAA+GLLVLYI IN+FK+YYG+DWEGLF+ITGYGLGGSSMALF

Sbjct: 184

KAFITAFRSGAVMGFLLAANGLLVLYIAINLFKLYYGEDWEGLFESITGYGLGGSSMALF 243

Query: 245

GRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDFGSYA 304

GRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDFGSYA

Sbjct: 244

GRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDFGSYA 303

Query: 305 EASCAALVVASISSFGINHDFTAMCYPLLISSMGLVCLITTLFATDFFEIKLVKEIEPA
364

E+SCAALVV ISSFGINHDFTAM YPLLISS+GILVCLITTLFATDFFEIK VKEIEPA

Sbjct: 304 ESSCAALVVPISSFGINHDFTAMLYPLLISSVGILVCLITTLFATDFFEIKAVKEIEPA
363

Query: 365 LKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVGVLWAGLIIGF
424

LK QLIISTV+MTVGIAIV+W+GLP+SFTIFNFGTQKVVKNWQLFLCV VGLWAGLIIGF

Sbjct: 364 LKKQLIISTVLMVTGIAIVTWIGLPSSFTIFNFGTQKVVKNWQLFLCVAVGLWAGLIIGF
423

Query: 425

VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXXMY 484

VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK MY

Sbjct: 424 VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSIIPIFAIAIGIFVSFSFAAMY
483

Query: 485

GVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTAAIG 544

G+AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTAAIG

Sbjct: 484

GIAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTAAIG 543

Query: 545

KGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAUTMKSVGSA 604

KGFAGSAALVSLALFGAFVSRA I TVDVLTPKV IGL+VGAMLPYWFSAUTMKSVGSA

Sbjct: 544

KGFAIGSAALVSLALFGAFVSRAISITVDVLTPKVFIGLIVGAMLPYWFSAUTMKSVGSA 603

Query: 605

ALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEIMPAGCLVMLTPLIVGFFF 664

ALKMVEEVRRQFNTIPGLMEG AKPDYATCVKISTDASIKEIMPAG LVMLTPLIVG FF

Sbjct: 604

ALKMVEEVRRQFNTIPGLMEGHAKPDYATCVKISTDASIKEIMPAGALVMLTPLIVGTFF 663

Query: 665

GVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHKAAV 724
GVETLSGVLAG+LVSGVQIAISASNTGGAWDNAKKYIEAG SEHA++LGPKGS+PHKAAV

Sbjct: 664

GVETLSGVLAGALVSGVQIAISASNTGGAWDNAKKYIEAGASEHARTLGPKGSDPHKAAV 723

Query: 725 IGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

IGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGG+LFK F

Sbjct: 724 IGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGLLFKMF 769

>gi|2827755|sp|P21616|AVP3_PHAAU Pyrophosphate-energized vacuolar membrane proton pump
(Pyrophosphate-energized inorganic pyrophosphatase)
(H+-PPase) (Vacuolar H+-pyrophosphatase)
gi|7436048|pir||T10841 inorganic diphosphatase (EC 3.6.1.1) - mung bean
gi|951323|gb|AAC49175.1| pyrophosphatase
Length = 765

Score = 1171 bits (3030), Expect = 0.0

Identities = 638/769 (82%), Positives = 681/769 (88%), Gaps = 4/769 (0%)

Query: 2 VAPALLPELWTEILVPICAVIGIAFSLFQWYVVSRVKLTSDLXXXXXXXXXXXXDY
61

+ A+LP+L TEIL+P+CAVIGIAF+LFQW +VS+VKL++ DY

Sbjct: 1 MGAAILPDLGTEILIPCAVIGIAFALFQWLLVSKVKLSA--VRDASPAAA
KNGYNDY 57

Query: 62

LIEEEEGVNDQSVVAKCAEIQTaisegatsflfteykyxxxxxxxxxxxxxLGSVEGF 121
LIEEEEG+ND +VV KCAEIQ AISEGATSFLTEYKY LGSVEGF

Sbjct: 58 LIEEEEGINDHNVVVKCAEIQNAISEGATSFLTEYKYVGIFMVAFAILIFLFLGSVEGF
117

Query: 122

STDNKPCTYDTRRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARK 181

ST + C+YD T+TCKPALATA FST++F+LG VTS++SGFLGMKIATYANARTTLEARK

Sbjct: 118

STSPQACSYDKTKPALATAIFSTVSFLGGVTSLVSGFLGMKIATYANARTTLEARK 177

Query: 182

GVGKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSM 241

 GVGKAFI AFRSGAVMGFLAA+GLLVLYI IN+FKIYYGDDW GLFEAITGYGLGGSSM

Sbjct: 178

GVGKAFITAFRSGAVMGFLAANGLLVLYIAINLFKIYYGDDWGLFEAITGYGLGGSSM 237

Query: 242

ALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAPIADNVGNDVGDIAGMGSDLFG 301

 ALFGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAPIADNVGNDVGDIAGMGSDLFG

Sbjct: 238

ALFGRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAPIADNVGNDVGDIAGMGSDLFG 297

Query: 302 SYAEASCAALVVASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEI

361

 SYAE+SCAALVVASISSFG+NH+ TAM YPL++SS+GILVCL+TTLFATDFFEIK VKEI

Sbjct: 298 SYAESSCAALVVASISSFGLNHELTAMLYPLIVSSVGILVCLLTLFATDFFEIKAVKEI

357

Query: 362

EPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVGWLWAGLI 421

 EPALK QL+ISTV+MT+G+A+VS+V LPTSFTIFNFG QK VK+WQLFLCV VGLWAGLI

Sbjct: 358

EPALKKQLVISTVLMТИGVAVVSFVALPTSFTIFNFGVQKDVKSWQLFLCVAVGLWAGLI 417

Query: 422

IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXX 481

 IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 418 IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSIIPIFAIAISIFVSFTFA

477

Query: 482

XMYGVAVAALGMLTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTTA 541

 MYG+AVAALGMLTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTTA

Sbjct: 478

AMYGIAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTTA 537

Query: 542

AIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKSV 601

AIGKGFAIGSAALVSLALFGAFVSRA I TVDVLTPKV IGL+VGAMLPYWFSAMTMKSV

Sbjct: 538 AIGKGFAIGSAALVSLALFGAFVSRSITTVDLTPKFIGLIVGAMLPYWFSAMTMKSV
597

Query: 602

GSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVG 661

GSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPG LVMLTPL+VG

Sbjct: 598

GSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGALVMLTPLVVG 657

Query: 662

FFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHK 721

FGVETLSGVLAGSLVSGVQIAISASNT GAWDNAKKYIEAG SEHA+SLGPKGS+ HK

Sbjct: 658 ILFGVETLSGVLAGSLVSGVQIAISASNT-
GAWDNAKKYIEAGASEHARSLGPKGSDCHK 716

Query: 722 AAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

AAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGG+LFK F

Sbjct: 717 AAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGLLFKIF 765



>gi|41023649|emb|CAF18416.1| proton translocating pyrophosphatase [Oryza sativa]

Length = 762

Score = 1140 bits (2949), Expect = 0.0

Identities = 620/766 (80%), Positives = 666/766 (86%), Gaps = 5/766 (0%)

Query: 5 ALLPELWTEILVPICAVIGIAFSLFQWYVVSRVKLTSDLXXXXXXXXXXXXXXDYLIE
64

A+L ++ TE+L+PI A+IGI FS+ QW +V+RVKL

D LIE

Sbjct: 2 AILSDVATEVLPIAAIIGFSIAQWVLVARVKLAPS----QPGASRSKDGYGDLSIE 56

Query: 65

EEEGVNDQSVVAKCAEIQTASEGATSFLTEYKYXXXXXXXXXXXXXXLGSVEGFSTD 124

EEEG+ND +VVAKCAEIQ AI+EGATSFLTEY+Y LGSVEGFST

Sbjct: 57 EEEGLNDHNVVAKCAEIQNAAEAGATSFLTEYQYVGVFMSIFAVVIFLFLGSVEGFSTK
116

Query: 125

NKPCTYDTRCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGVG 184

PCTY + CKPAL A FST++F+LGA+TSV+SGFLGMKIATYANARTTLEARKGVG

Sbjct: 117

THPCTYSKDKECKPALFNALFSTVSFLGAITSVSGFLGMKIATYANARTTLEARKGVG 176

Query: 185

KAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSMALF 244

KAFI AFRSGAVMGFLA++GLLVLYI IN+FK+YYGDDWEGLFE+ITGYGLGGSSMALF

Sbjct: 177

KAFITAFRSGAVMGFLASNGLLVLYIAINLFMYYGDDWEGLFESITGYGLGGSSMALF 236

Query: 245

GRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAPIADNVGDNVGDIAFMGSDFGSYA 304

GRVGGGIYTKAADVGA LVGK+ERNIPEDDPRNPAPIADNVGDNVGDIAFMGSDFGSYA

Sbjct: 237

GRVGGGIYTKAADVGAGLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAFMGSDFGSYA 296

Query: 305 EASCAALVVASISSFGINHDFTAMCYPLLISSMGLVCLITTLFATDFFIEKLVKEIEPA

364

E+SCAALVVASISSFGINHDFT MCYPLL+SSMGI+VCLITTLFATDFFIEIK VKEIEP+

Sbjct: 297 ESSCAALVVASISSFGINHDFTGMCYPLLVSSMGIIVCLITTLFATDFFIEIKAVKEIEPS

356

Query: 365 LKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVGLWAGLIIGF

424

LK QLIIST +MTVGIA+VSW+ LP FTIFNFG QK V NW LFLCV +GLWAGLIIG+

Sbjct: 357 LKKQLIISTALMTVGIALVSWLALPYKFTIFNFGEQKEVTNWGLFLCVSIGLWAGLIIGY

416

Query: 425

VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXMY 484

VTEYYTSNAYSPVQDVAD+CRTGAATNVIFGLALGYK MY

Sbjct: 417 VTEYYTSNAYSPVQDVADACRTGAATNVIFGLALGYKSVIPIFAIALGIYVSFTIAAMY
476

Query: 485

GVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTAAIG 544

G+AVAALGMLSTIATGL+IDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTAAIG

Sbjct: 477

GIAVAALGMLSTIATGLSIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTAAIG 536

Query: 545

KGFAIGSAALVSLALFGAFVSRAFIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKSVGSA 604

KGFAIGSAALVSLALFGAFVSRAF+ VDVL+PKVIIGL+VGAMLPYWFSAMTMKSVGSA

Sbjct: 537

KGFAIGSAALVSLALFGAFVSRAFKVVDVLSPKVIIGLIVGAMLPYWFSAMTMKSVGSA 596

Query: 605

ALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFFF 664

ALKMVEEVRRQFNTIPGLMEGT KPDY A CVKISTDASIK+MIPPG LVMLTPLIVG F

Sbjct: 597

ALKMVEEVRRQFNTIPGLMEGTGKPDYANCVKISTDASIKQMIPPGALVMLTPLIVGTLF 656

Query: 665

GVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHKAAV 724

GV+TLSGVLAG+LVSGVQ+AISASNTGGAWDNAKKYIEAG SEHA+SLGPKGS+ HKAAV

Sbjct: 657

GVQTLSGVLAGALVSGVQVAISASNTGGAWDNAKKYIEAGASEHARSLGPKGSDCHKAAV 716

Query: 725 IGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

IGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFK F

Sbjct: 717 IGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKLF 762

>gi|38045977|gb|AAR08913.1| pyrophosphate-energized vacuolar membrane proton pump
[Thellungiella salsuginea]
Length = 771

Score = 1279 bits (3310), Expect = 0.0

Identities = 695/771 (90%), Positives = 708/771 (91%), Gaps = 1/771 (0%)

Query: 1 MVAPALLPELWTEILVPICAVIGIAFSLFQWYVSRVKLTSD-LXXXXXXXXXXXXXX
59

MVA A LPELWTEILVP+CAVIGIAFSLFQW++VSrv++T+D

Sbjct: 1

MVASAFLPELWTEILVPVCAVIGIAFSLFQWFIVSRVRTADQGASSSSGGSNNGKNGYG 60

Query: 60

DYLIEEEEGVNDSVVAKCAEIQTASEGATSLFTEYKYXXXXXXXXXXXXXLSVE 119

DYLIEEEEG+N+QSvVAKCAEIQTASEGATSLFTEYKY LGSVE

Sbjct: 61 DYLIEEEGLNEQSvVAKCAEIQTASEGATSLFTEYKYVGFMVFAAIIFVFLGSVE
120

Query: 120

GFSTDNKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEA 179

GFST NKPCTYD T+TCKPALATAAFST+AFVLGAVTSVLSGFLGMKIATYANARTTLEA

Sbjct: 121

GFSTKNKPCTYDDTKCKPALATAAFSTVAFVLGAVTSVLSGFLGMKIATYANARTTLEA 180

Query: 180

RKGVGKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGS 239

RKGVGKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIY BDWEGLFEAITGYGLGGS

Sbjct: 181

RKGVGKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYXXBDWEGLFEAITGYGLGGS 240

Query: 240

SMALFGRVGGGIYTKAADVGADELVGKIERNIPEDDPRNPAPIADNVGDNVGDAGMGSDL 299

SMALFGRVGGGIYTKAADVGADELVGKIERNIPEDDPRNPAPIADNVGDNVGDAGMGSDL

Sbjct: 241

SMALFGRVGGGIYTKAADVGADELVGKIERNIPEDDPRNPAPIADNVGDNVGDAGMGSDL 300

Query: 300 FGSYAEASCAA
VVASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVK
359

FGSYAEASCAA
VVASISSFGINHDFTAM YPLLISSMGILVCLITTLFATDFFEIK VK
Sbjct: 301 FGSYAEASCAA
VVASISSFGINHDFTAMLYPPLIISMGILVCLITTLFATDFFEIKAVK
360

Query: 360

EIEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAG 419
EIEPALKNQLIISTVIMTVGIAIVSWVGLP+SFTIFNFGTQKVVKNWQLFLCVCVGLWAG
Sbjct: 361 EIEPALKNQLIISTVIMTVGIAIVSWVGLPSSFTIFNFGTQKVVKNWQLFLCVCVGLWAG
420

Query: 420

LIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXX 479
LIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK
Sbjct: 421 LIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAASIFVSFS
480

Query: 480

XXXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNT 539
MYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNT
Sbjct: 481
FAAMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNT 540

Query: 540

TAAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMK 599
TAAIGKGFAIGSAALVSLALFGAFVSRA+HTVDVLTPKVIIGLLVGAMLPYWFSAMTMK
Sbjct: 541
TAAIGKGFAIGSAALVSLALFGAFVSRAGVHTVDVLTPKVIIGLLVGAMLPYWFSAMTMK 600

Query: 600

SVGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEIMP
GCLVMLTPLI 659
SVGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEIMP
GCLVMLTPLI
Sbjct: 601
SVGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEIMP
GCLVMLTPLI 660

Query: 660

VGFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEP 719
VGFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEP

Sbjct: 661

VGFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEP 720

Query: 720 HKAavigdtigdplkdtsgpslniliklmaveslvfapffathggilfkY 770

HKAavigdtigdplkdtsgpslniliklmaveslvfapffathggilfkY

Sbjct: 721 HKAavigdtigdplkdtsgpslniliklmaveslvfapffathggilfkYL 771

>gi|38488590|dbj|BAD02277.1| vacuolar proton pyrophosphatase [Oryza sativa (japonica cultivar-group)]
Length = 770

Score = 1175 bits (3039), Expect = 0.0

Identities = 638/770 (82%), Positives = 676/770 (87%)

Query: 1

MVAPALLPELWTEILVPICAVIGIAFSLFQWYVSRVKLTSDLXXXXXXXXXXXXXXD 60
M A A+LPEL +++++P+ A +GIAF++ QW +VS+VKLT++ D

Sbjct: 1

MAAAAILPELAQVVIPVAAAVGIAFAVLQWALVSKVKLTAEPRRGAEAGGAAGGKSGPSD 60

Query: 61

YLIEEEEVGNDQSVAKCAEIQTASEGATSFLTEYKYXXXXXXXXXXXXXLGSVEG 120
YLIEEEEGLNDHNVSKCAEIQTASEGATSFLTEYKYVGLFMSIFAVLIFLFLGSVEG
Sbjct: 61 YLIEEEEGLNDHNVSKCAEIQTASEGATSFLTEYKYVGLFMSIFAVLIFLFLGSVEG
120

Query: 121

FSTDNKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEAR 180
FST ++PC Y +TCKPALA A FSTIAFVLGAVTS++SGFLGMKIATYANARTTLEAR

Sbjct: 121

FSTKSQPCHYSKDTCKPALANAIFSTIAFVLGAVTSVSGFLGMKIATYANARTTLEAR 180

Query: 181

KVGKAFIAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS 240

KVGKAFI AFRSGAVMGFLAASGLLVLYI IN+F IYYGDDWEGLFEAITGYGLGGSS

Sbjct: 181

KVGKAFITAFRSGAVMGFLAASGLLVLYIANLFGIYYGDDWEGLFEAITGYGLGGSS 240

Query: 241

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAPIADNVGDNVGDAGMGSDLF 300

MALFGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAPIADNVGDNVGDAGMGSDLF

Sbjct: 241

MALFGRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAPIADNVGDNVGDAGMGSDLF 300

Query: 301 GSYAEASCAA VVASISSFGINHDFTAMCYPLLISSM GILVCLITTLFATDFFEIKLVKE

360

GSYAE+SCAALVVASISSFGINH+FT M YPLL+SS+GI+ CLITTLFATDFFEIK V E

Sbjct: 301 GSYAE SCAA VVASISSFGINHEFTP MVYPLL VSSV GIACLITTLFATDFFEIKAVSE

360

Query: 361

IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVVGLWAGL 420

IEPALK QLIIST MTVGIA+VSW+GLP +FTIFNFG QK V++WQLFLCV VGLWAGL

Sbjct: 361

IEPALKKQLIISTAFMTVGIALVSWLGLPYTFTIFNFGAQKTVQSWQLFLCVAVGLWAGL 420

Query: 421

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXX 480

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 421 IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAFSIFLSFSL

480

Query: 481

XXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT 540

MYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT

Sbjct: 481

AAMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT 540

Query: 541

AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKS 600

AAIGKGFAIGSAALVSLALFGAFVSRA I TVDVLTpv IGL+VGAMLPYWFSAMTMKS

Sbjct: 541

AAIGKGFAIGSAALVSLALFGAFVSRAAISTVDVLTPKVFIGLIVGAMLPYWFSAMTMKS 600

Query: 601

VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV 660

VGSAALKMVEEVRRQFNTIPGLMEGT KPDYATCVKISTDASIKEMIPPG LVMLTPLIV

Sbjct: 601

VGSAALKMVEEVRRQFNTIPGLMEGTTKPDYATCVKISTDASIKEMIPPGALVMLTPLIV 660

Query: 661

GFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPH 720

G FGVETLSGVLAG+LVSGVQIAISASNTGGAWDNAKKYIEAG S HA++LGPKGS+PH

Sbjct: 661

GILFGVETLSGVLAGALVSGVQIAISASNTGGAWDNAKKYIEAGASGHARTLGPKGSDPH 720

Query: 721 KAAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

KAAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFK F

Sbjct: 721 KAAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKLF 770

>gi|2129949|pir|S61422 inorganic diphosphatase (EC 3.6.1.1) (clone TVP5) - common tobacco

Length = 764

Score = 1190 bits (3078), Expect = 0.0

Identities = 642/769 (83%), Positives = 680/769 (88%), Gaps = 5/769 (0%)

Query: 2 VAPALLPELWTEILVPICAVIGIAFSLFQWYVVSRVKLTSDLXXXXXXXXXXXXDY

61

+ ALLP+L T+I++P+CAVIGI FS FQWY+VSrvk++S+

D

Sbjct: 1

MGSALLPDLGTQIVIPVCAVIGIVFSSFWYLVSERVKSSEHGATSPSSNKNKNGYGD 60

Query: 62

LIEEEEGVNDQSVVAKCAEIQTaisegatsflfTEYKYXXXXXXXXXXXXXXLGSVEGF 121

LIEEEEG+ND +VVAKCA+IQ AISEGATSLFLTEY+Y LGSVEGF

Sbjct: 61 LIEEEEGINDHNWAKCADIQNAISEGATSLFLTEYQYVGIFMIAFAILIFLFLGSVEGF
120

Query: 122

STDNKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARK 181

ST ++PCTY+ + CKPALATA FST++F+LGA+TSV+SGFLGMKIATYANARTTLEARK

Sbjct: 121 STSSQPCTYNKEKRCKPALATAIFSTVSFLLGAITSVISGFLGMKIATYANARTTLEARK
180

Query: 182

GVGKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSM 241

GVGKA +V VMGFLLAA+GLLVLYI IN+FK+YYGDDWEGLFEAITGYGLGGSSM

Sbjct: 181 GVGKACLVQ----VMGFLLAANGLLVLYIAINLFKLYYGDWEGLFEAITGYGLGGSSM
235

Query: 242

ALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPRAVIADNVGDNVGDIA GMGSDLFG 301

ALFGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPRAVIADNVGDNVGDIA GMGSDLFG

Sbjct: 236

ALFGRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPRAVIADNVGDNVGDIA GMGSDLFG 295

Query: 302 SYAEASCAA VVASISSFGI+HDFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEI
361

SYAE+SCAALVVASISSFGI+HDFTAMCYPLLISSMGILVCLITTLFATDFFEIK VKEI

Sbjct: 296 SYAESSCAA VVASISSFGIDHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKAVKEI
355

Query: 362

EPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVVGLWAGLI 421

EPALKNQLIIST IMTVGIAIV+W LP+SFTIFNFGTQKVVKNWQLFLCV VGLWAGLI

Sbjct: 356 EPALKNQLIISTAIMTVGIAVTWTCLPSSFTIFNFGTQKVVKNWQLFLCVAVGLWAGLI
415

Query: 422

IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXX 481
IGFVTEYYTSNAYSPVQDVADSC TGAATNVIFGLALGYK

Sbjct: 416 IGFVTEYYTSNAYSPVQDVADSCSTGAATNVIFGLALGYKSVIPIFAIAIAIFVSFTFA
475

Query: 482

XMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTTA 541
M +AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTTA

Sbjct: 476

AMGYIAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTTA 535

Query: 542

AIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKSV 601
AIGKGFAIGSAALVSLALFGAFVSRAGI TVDVLTP+V IGL+VGAMLPYWFSAMTMKSV

Sbjct: 536

AIGKGFAIGSAALVSLALFGAFVSRAGISTVDVLTPQVFIGLIVGAMLPYWFSAMTMKSV 595

Query: 602

GSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVG 661
GSAALKMVEEVRRQFNTIPGLMEG AKPDYATCVKISTDASIKEMIPPG LVMLTPLIVG

Sbjct: 596

GSAALKMVEEVRRQFNTIPGLMEGLAKPDYATCVKISTDASIKEMIPPGALVMLTPLIVG 655

Query: 662

FFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHK 721
FFGVETLSGVLAG+LVSGVQIAISASNTGGAWDNAKKYIEAG SEHA++LGPKGSEPHK

Sbjct: 656

IFFGVETLSGVLAGALVSGVQIAISASNTGGAWDNAKKYIEAGASEHARTLGPKGSEPHK 715

Query: 722 AAVIGDTIGDPLKDTGPSLNILIKLMAVESL VFAPFFATHGGILFKYF 770

AAVIGDTIGDPLKDTGPSLNILIKLMAVESL VFAPFFATHGGILFK F

Sbjct: 716 AAVIGDTIGDPLKDTGPSLNILIKLMAVESL VFAPFFATHGGILFKIF 764

□ >gi|18274925|sp|Q06572|AVP3_HORVU Pyrophosphate-energized vacuolar membrane proton pump

(Pyrophosphate-energized inorganic pyrophosphatase)

(H+-PPase)

gi|6012172|dbj|BAA02717.2| inorganic pyrophosphatase [Hordeum vulgare subsp. vulgare]

Length = 762

Score = 1153 bits (2983), Expect = 0.0

Identities = 624/765 (81%), Positives = 671/765 (87%), Gaps = 5/765 (0%)

Query: 5 ALLPELWTEILVPICAVIGIAFSLFQWYVVSRVKLTSDLXXXXXXXXXXXXXXDYLIE
64

A+L EL TEIL+P+C VIGI F++ QW++VS+VK+T DYLIE

Sbjct: 2 AILGELGTEILIPVCGVIGIVFAVAQWFIVSKVKVTPGAASAAAGAKNGYG---DYLIE 57

Query: 65

EEEGVNDQSVVAKCAEIQTASEGATSFLTEYKYXXXXXXXXXXXXXLSVEGFSTD 124

EEEG+ND +VV KCAEIQTASEGATSFLFT Y+Y LGS+EGFST

Sbjct: 58 EEEGLNDHNVVVKCAEIQTASEGATSFLFTMYQYVGMFMVVFAAIIFLFLGSIEGFSTK
117

Query: 125

NKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGVG 184

+PCTY + TCKPAL TA FST +F+LGA+TS++SGFLGMKIATYANARTTLEARKGVG

Sbjct: 118 GQPCTY-

SKGTCKPALYTALFSTASFLLGAITSLVSGFLGMKIATYANARTTLEARKGVG 176

Query: 185

KAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEITGYGLGGSSMALF 244

KAFI AFRSGAVMGFL++SGL+VLYITINVFK+YYGDDWEGLFE+ITGYGLGGSSMALF

Sbjct: 177

KAFITAFRSGAVMGFLSSSGLVVLYITINVFKMYYGDDWEGLFESITGYGLGGSSMALF 236

Query: 245

GRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYA 304

GRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYA

Sbjct: 237

GRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYA 296

Query: 305 EASCAALVVASISSFGINHDFTAMCYPLLISSMGLVCLITTLFATDFFEIKLVEIEPA

364

E+SCAALVVASISSFGINHDFTAMCYPLL+SS+GI+VCL+TTLFATDFFEIK EIEPA

Sbjct: 297 ESSCAALVVASISSFGINHDFTAMCYPLLSSVGIIVCLLTLFATDFFEIKAAANEIEPA

356

Query: 365 LKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGLIIGF

424

LK QLIIST +MTVG+A++SW+ LP FTIFNFG QK V NW LF CV VGLWAGLIIGF

Sbjct: 357 LKKQLIISTALMTVGAVISWLALPAKFTIFNFGAQKEVSNWGLFFCVAVGLWAGLIIGF

416

Query: 425

VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXXMY 484

VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK MY

Sbjct: 417 VTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAVSIYVSFSIAAMY

476

Query: 485

GVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRIRERTDALDAAGNTAAIG 544

G+A+AALGMLST+ATGLAIDAYGPISDNAGGIAEMAGMSHIRIRERTDALDAAGNTAAIG

Sbjct: 477

GIAMAALGMLSTMATGLAIDAYGPISDNAGGIAEMAGMSHIRIRERTDALDAAGNTAAIG 536

Query: 545

KGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKSVGSA 604

KGFAIGSAALVSLALFGAFVSrag+ VDVL+PKV IGL+VGAMLPYWFSAMTMKSVGSA

Sbjct: 537

KGFAIGSAALVSLALFGAFVSragVKVVDSLSPKVFIGLIVGAMLPYWFSAMTMKSVGSA 596

Query: 605

ALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFFF 664

ALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPG LVMLTPLIVG F

Sbjct: 597

ALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGALVMLTPLIVGTLF 656

Query: 665

GVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHKA AV 724

GVETLSGVLAG+LVSGVQIAISASNTGGAWDNAKKYIEAG SEHA+SLGPKGS+ HKAAV

Sbjct: 657

GVETLSGVLAGALVSGVQIAISASNTGGAWDNAKKYIEAGNSEHARSLGPKGSDCHKA AV 716

Query: 725 IGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKY 769

IGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFAT+GG+LFKY

Sbjct: 717 IGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATYGGLLFKY 761



>gi|7436043|pir||T07801 probable inorganic diphosphatase (EC 3.6.1.1) - mung bean

gi|2653446|dbj|BAA23649.1| proton pyrophosphatase [Vigna radiata]

Length = 766

Score = 1178 bits (3047), Expect = 0.0

Identities = 639/769 (83%), Positives = 682/769 (88%), Gaps = 3/769 (0%)

Query: 2 VAPALLPELWTEILVPICAVIGIAFSLFQWYVVSRVKLTSDLXXXXXXXXXXXXDY
61

+ A+LP+L TEIL+P+CAVIGIAF+LFQW +VS+VKL++ DY

Sbjct: 1 MGAAILPDLGTEILIPCAVIGIAFALFQWLLSKVKLSA--VRDASPNAAKNGYNDY 57

Query: 62

LIEEEEGVNDQSVVAKCAEIQTaisegatsflfteykyXXXXXXXXXXXXXXLGSVEGF 121

LIEEEEG+ND +VV KCAEIQ AISEGATSFLFTEYKY LGSVEGF

Sbjct: 58 LIEEEEGINDHNVVVKCAEIQNaisegatsflfteykyvgifmvaFAILIFLFLGSVEGF

117

Query: 122

STDNKPCTYDTRRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARK 181
ST + C+YD T+TCKPALATA FST++F+LG VTS++SGFLGMKIATYANARTTLEARK

Sbjct: 118

STSPQACSYDKTKTCKPALATAIFSTVSFLLGGVTSLVSGFLGMKIATYANARTTLEARK 177

Query: 182

GVGKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSM 241

GVGKAFI AFRSGAVMGFLAA+GLLVLYI IN+FKIYYGDDW GLFEAITGYGLGGSSM

Sbjct: 178

GVGKAFITA FRSGAVMGFLAANGLLVLYIAINLFKIYYGDDWGGLFEAITGYGLGGSSM 237

Query: 242

ALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAPIADNVGDNVGDIAGMGSDLFG 301

ALFGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAPIADNVGDNVGDIAGMGSDLFG

Sbjct: 238

ALFGRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAPIADNVGDNVGDIAGMGSDLFG 297

Query: 302 SYAEASCAALVVASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEI

361

SYAE+SCAALVVASISSFG+NH+ TAM YPL++SS+GILVCL+TTLFATDFFEIK VKEI

Sbjct: 298 SYAESSCAALVVASISSFGLNHELTAMLYPLIVSSVGILVCLLTTLFATDFFEIKAVKEI

357

Query: 362

EPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVKNWQLFLCVCGWLWAGLI 421

EPALK QL+ISTV+MT+G+A+VS+V LPTSFTIFNFG QK VK+WQLFLCV VGLWAGLI

Sbjct: 358

EPALKKQLVISTVLMТИGVAVSFVALPTSFTIFNFGVQKDVKSWQLFLCVAVGLWAGLI 417

Query: 422

IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXX 481

IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 418 IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAISIFVSFTLA

477

Query: 482

XMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTTA 541
MYG+AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTTA

Sbjct: 478

AMYGIAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTTA 537

Query: 542

AIGKGFAIGSAALVSLALFGAFVSRA|TVDVLPKV IGL+VGAMLPYWFSAMTMKSV 601
AIGKGFAIGSAALVSLALFGAFVSRA|TVDVLTPKV IGL+VGAMLPYWFSAMTMKSV
Sbjct: 538 AIGKGFAIGSAALVSLALFGAFVSRA|TVDVLTPKV FIGLIVGAMLPYWFSAMTMKSV
597

Query: 602

GSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVG 661
GSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPG LVMLTPL+VG
Sbjct: 598
GSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPG GALVMLTPLVVG 657

Query: 662

FFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHK 721
FGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAG SEHA+SLGPKGS+ HK
Sbjct: 658
ILFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGASEHARSLGPKGSDCHK 717

Query: 722 AAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

AAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGG+LFK F
Sbjct: 718 AAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGLLFKIF 766

>gi|15218279|ref|NP_173021.1| pyrophosphate-energized vacuolar membrane proton pump /
pyrophosphate-energized inorganic pyrophosphatase
(AVP-3) [Arabidopsis thaliana]
gi|399091|sp|P31414|AVP3_ARATH Pyrophosphate-energized vacuolar membrane proton pump

(Pyrophosphate-energized inorganic pyrophosphatase)

(H+-PPase)

gi|282878|pir|A38230 inorganic diphosphatase (EC 3.6.1.1), H+-translocating
pyrophosphate-energized - *Arabidopsis thaliana*

gi|166634|gb|AAA32754.1| vacuolar H+-phosphatase

gi|8927648|gb|AAF82139.1| Identical to Vacuolar proton pyrophosphatase (AVP3) from
Arabidopsis thaliana gb|AB015138 and gb|M81892. ESTs
gb|AA006922, gb|AA586042, gb|AA651053, gb|AA712863,
gb|AA394384, gb|AA605347, gb|AA006474, gb|AA006772,
gb|AA650817, gb|AA042538, gb|AA006217, gb|AW004149,
gb|H36252, gb|H36659, gb|R30444, gb|W43600, gb|W43886,
gb|W43517, gb|W43127, gb|N96656, gb|T14167, gb|T76140,
gb|T21188, gb|Z17694, gb|Z17695 come from this gene

gi|27311751|gb|AAO00841.1| Unknown protein [*Arabidopsis thaliana*]

Length = 770

Score = 1316 bits (3405), Expect = 0.0

Identities = 718/770 (93%), Positives = 718/770 (93%)

Query: 1

MVAPALLPELWTEILVPICAVIGIAFSLFQWYVVSRVKLTSDLXXXXXXXXXXXXXXD 60

MVAPALLPELWTEILVPICAVIGIAFSLFQWYVVSRVKLTSDL D

Sbjct: 1

MVAPALLPELWTEILVPICAVIGIAFSLFQWYVVSRVKLTSDLGASSGGANNGKNGYGD 60

Query: 61

YLIIEEEGVNDQSVVAKCAEIQTASEGATSFLTEYKYXXXXXXXXXXXXXLGSVEG 120

YLIIEEEGVNDQSVVAKCAEIQTASEGATSFLTEYKY LGSVEG

Sbjct: 61 YLIIEEEGVNDQSVVAKCAEIQTASEGATSFLTEYKYVGVFMIFFAAVIFVFLGSVEG
120

Query: 121

FSTDNKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEAR 180

FSTDNKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEAR

Sbjct: 121

FSTDNKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEAR 180

Query: 181

KVGKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS 240
KVGKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS

Sbjct: 181

KVGKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS 240

Query: 241

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAFMGSDF 300
MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAFMGSDF

Sbjct: 241

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAFMGSDF 300

Query: 301 GSYAEASCAALVVASISSFGINHDFTAMCYPLLISSMGLVCLITTLFATDFFEIKLVKE
360

GSYAEASCAALVVASISSFGINHDFTAMCYPLLISSMGLVCLITTLFATDFFEIKLVKE
Sbjct: 301 GSYAEASCAALVVASISSFGINHDFTAMCYPLLISSMGLVCLITTLFATDFFEIKLVKE
360

Query: 361

IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGL 420
IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGL
Sbjct: 361 IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGL
420

Query: 421

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXX 480
IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGY
Sbjct: 421 IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAISIFVSFSF
480

Query: 481

XXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTT 540
MYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTT
Sbjct: 481
AAMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTT 540

Query: 541

AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKS 600
AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKS

Sbjct: 541

AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKS 600

Query: 601

VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV 660

VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV

Sbjct: 601

VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV 660

Query: 661

GFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPH 720

GFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPH

Sbjct: 661

GFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPH 720

Query: 721 KAAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

KAAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF

Sbjct: 721 KAAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770



>gi|1076627|pir|S54172 inorganic diphosphatase (EC 3.6.1.1) - common tobacco

gi|790479|emb|CAA58701.1| inorganic pyrophosphatase [Nicotiana tabacum]

Length = 765

Score = 1203 bits (3113), Expect = 0.0

Identities = 650/769 (84%), Positives = 686/769 (89%), Gaps = 4/769 (0%)

Query: 2 VAPALLPELWTEILVPICAVIGIAFSLFQWYVVSRVKLTSDLXXXXXXXXXXXXXXDY

61

+ ALLP+L E|++P+CAVIGI FSL QWY+VS VKLT + DY

Sbjct: 1 MGAALLPDLGAEIVIPVCAVIGIVFSLVQWYLVSNVKLTPE----SSPSNNGKNGYGDY

56

Query: 62

LIEEEEGVNDQSVAKCAEIQTaisegatsflfTEYKYXXXXXXXXXXXXXXLGSVEGF 121

LIEEEEG+N+Q+VV KCAEIQ AISEGATSLFTEY+Y LGSVEGF

Sbjct: 57 LIEEEEGINEQNWWKCAEIQNAISEGATSLFTEYQYVGIFMIAFAILIFLFLGSVEGF
116

Query: 122

STDNKPCTYDTRTRCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARK 181

ST ++PCTY+ + CKPALATA FST++F+LGAVTSV+SGFLGMKIATYANARTTLEARK

Sbjct: 117

STKSQPCTYNKEKLCKPALATAIFSTVSFLGAVTSVSGFLGMKIATYANARTTLEARK 176

Query: 182

GVGKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSM 241

GVGKAFIVAFRSGAVMGFLAA+GLLVLYI IN+FK+YYGDDWEGLFEAITGYGLGGSSM

Sbjct: 177

GVGKAFIVAFRSGAVMGFLAANGLLVLYIAINLFKLYYGDDWEGLFEAITGYGLGGSSM 236

Query: 242

ALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAPIADNVGDNVGDAGMGSDLFG 301

ALFGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAPIADNVGDNVGDAGMGSDLFG

Sbjct: 237

ALFGRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAPIADNVGDNVGDAGMGSDLFG 296

Query: 302 SYAEASCAA LVVASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEI

361

SYAEASCAA LVVASISSFGINH+FTAM YPLLISSMGIL+CLITTLFATDFFEIK VKEI.

Sbjct: 297 SYAEASCAA LVVASISSFGINHEFTAMLYPLLISSMGILICLITTLFATDFFEIKAVKEI 356

Query: 362

EPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCGWLWAGLI 421

EPALKNQLIIST +MTVGIAIV+W LP+SFTIFNFG QKVVKNWQLFLCV VGLWAGLI

Sbjct: 357 EPALKNQLIISTALMTVGIAIVWTCLPSSFTIFNFGAQKVVKNWQLFLCVAVGLWAGLI
416

Query: 422

IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXX 481
IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 417 IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAIAIFVSFSFA
476

Query: 482

XMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTTA 541
MYG+AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTTA
Sbjct: 477

AMYGIAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTTA 536

Query: 542

AIGKGFAIGSAALVSLALFGAFVSRAGIHTVDLTPKVIIGLLVGAMLPYWFSAMTMKSV 601
AIGKGFAIGSAALVSLALFGAFVSRA I TVDVLTP+V IGL+VGAMLPYWFSAMTMKSV
Sbjct: 537

AIGKGFAIGSAALVSLALFGAFVSRAAITTVDLTPQVFIGLIVGAMLPYWFSAMTMKSV 596

Query: 602

GSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVG 661
GSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPG LVMLTPLIVG
Sbjct: 597

GSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGALVMLTPLIVG 656

Query: 662

FFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHK 721
FFGVETLSGVLAG+LVSGVQIAISASNTGGAWDNAKKYIEAG SEHA++LGPKGS+PHK
Sbjct: 657

IFFGVETLSGVLAGALVSGVQIAISASNTGGAWDNAKKYIEAGASEHARTLGPKGSDPHK 716

Query: 722 AAVIGDTIGDPLKDTGPSLNILIKLMAVESL VFAPFFATHGGILFKYF 770

AAVIGDTIGDPLKDTGPSLNILIKLMAVESL VFAPFFATHGG+LFK F

Sbjct: 717 AAVIGDTIGDPLKDTGPSLNILIKLMAVESL VFAPFFATHGGLLFKIF 765

>gi|19310433|gb|AAL84953.1| At1g15690/F7H2_3 [Arabidopsis thaliana]

Length = 770

Score = 1314 bits (3400), Expect = 0.0

Identities = 717/770 (93%), Positives = 717/770 (93%)

Query: 1

MVAPALLPELWTEILVPICAVIGIAFSLFWYVVSRVKLTSXLXXXXXXXXXXXXXXD 60

MVAPALLPELWTEILVPICAVIGIAFSLFWYVVSRVKLTS D

Sbjct: 1

MVAPALLPELWTEILVPICAVIGIAFSLFWYVVSRVKLTSDLGASSSGGANNGKNGYGD 60

Query: 61

YLIEEEEGVNDQSVVAKCAEIQTASEGATSFLTEYKYXXXXXXXXXXXXXLSVEG 120

YLIEEEEGVNDQSVVAKCAEIQTASEGATSFLTEYKY LGSVEG

Sbjct: 61 YLIEEEEGVNDQSVVAKCAEIQTASEGATSFLTEYKYGVFMIFAAVIFVFLGSVEG

120

Query: 121

FSTDNKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEAR 180

FSTDNKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEAR

Sbjct: 121

FSTDNKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEAR 180

Query: 181

KVGKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS 240

KVGKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS

Sbjct: 181

KVGKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS 240

Query: 241

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAPIADNVGDNVGDAGMGSDF 300

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAPIADNVGDNVGDAGMGSDF

Sbjct: 241

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAPIADNVGDNVGDAGMGSDF 300

Query: 301 GSYAEASCAALVVASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKE
360

GSYAEASCAALVVASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKE
Sbjct: 301 GSYAEASCAALVVASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKE
360

Query: 361

IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGL 420
IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGL
Sbjct: 361 IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGL
420

Query: 421

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXX 480
IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK
Sbjct: 421 IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIAISIFVSFSF
480

Query: 481

XXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTT 540
MYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTT
Sbjct: 481
AAMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTT 540

Query: 541

AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKS 600
AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKS
Sbjct: 541
AAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKS 600

Query: 601

VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV 660
VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV
Sbjct: 601
VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV 660

Query: 661

GFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPH 720
GFFFGVETLSGVLAGSLVSGVQIASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPH

Sbjct: 661

GFFFGVETLSGVLAGSLVSGVQIATSASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPH 720

Query: 721 KAAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

KAAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF

Sbjct: 721 KAAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

[gi|34894952|ref|NP_908801.1|](#) putative H+-pyrophosphatase [Oryza sativa (japonica cultivar-group)]
[gi|15290183|dbj|BAB63873.1|](#) putative H+-pyrophosphatase [Oryza sativa (japonica cultivar-group)]
Length = 773

Score = 994 bits (2569), Expect = 0.0

Identities = 545/768 (70%), Positives = 625/768 (81%), Gaps = 12/768 (1%)

Query: 13 EILVPICAVIGIAFSLFQWYVVSRVKLTS-----DLXXXXXXXXXXXXXXD 60
+ ++P CA +GIAF+++QW +VSRVK++

Sbjct: 6

DAVIPACAAVGIAFAWQWLLVSRVKVSPYSAAAAARNGGAGRAVFRPEGEVDDDDGGC 65

Query: 61

YLIEEEEGVNDQSVAKC AEIQTAISEGAT SFLTEYKYXXXXXXXXXXXXX LGSVEG 120
EE +G + +A+CAEIQ+AI GA SFLFT+YKY LGSV

Sbjct: 66

GDDEEADGDGGVAAMARCAEIQS AIRVGANSFLFTQYKYLAFTA VFAVVI FLFLGSVHR 125

Query: 121

FSTDNKPCTYDTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEAR 180
FST+++PC Y + CKPALA A FSTIAF+LGA TSV SGFLGM+IAT ANARTT+EAR

Sbjct: 126

FSTESQPCQYTRGKACKPALANAVFSTIAFLLGAAATSVASGFLGMRIATAANARTTVEAR 185

Query: 181

KGVGKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSS 240

+G+G AF AFRSGAVMGFLA+ GLLVLY+ I VF +YYGDDWEGL+E+ITGYGLGGSS

Sbjct: 186

RGIGPAFAAFRSGAVMGFLASLGLLVLYVAIKVFGLYYGDDWEGLYESITGYGLGGSS 245

Query: 241

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAPIADNVGDNVGDIAGMGSDLF 300

MALFGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAPIADNVGDNVGDIAGMGSDLF

Sbjct: 246

MALFGRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAPIADNVGDNVGDIAGMGSDLF 305

Query: 301 GSAYEASCAA LVV ASISSFGINHDFTAMCYPLLISSMGLVCLITLFATDFFEIKLVKE

360

GSYAE++CAAL V SISSFG +H+F A+ YPLLISS G++VCLITLFATD ++K V

Sbjct: 306 GSAYAESTCAALFVGSISSFGADHNFAAVSYPLLISSAGLIVCLITLFATDLYRVKTVDG

365

Query: 361

IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGL 420

+ PALK QL+ISTV+MTVG+ +V++ LP FT+F+FG K VKNW LF CV +GLWAGL

Sbjct: 366

VAPALKLQLLISTVLMTVGVLVVTFTALPHEFTMFDFGEVKRVKNWHLFFCVTIGLWAGL 425

Query: 421

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXX 480

IGF TEY+TSNAYSPV+DVADSCRTGAATNVIFGLALGYK

Sbjct: 426 AIGFTTEYFTSNAYSPVRDVADSCRTGAATNVIFGLALGYKSVIVPVFAIAVSIYVSFTL

485

Query: 481

XXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT 540

+YG+AVAALGMLST+ATGLAIDAYGPISDNAGGIAEMAGMSHRIR+RTDALDAAGNTT

Sbjct: 486

ASIYGIAVAALGMLSTVATGLAIDAYGPISDNAGGIAEMAGMSHIRQRTDALDAAGNTT 545

Query: 541

AAIGKGFAIGSAALVSLALFGAFVSRAFIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKS 600

AAIGKGFAIGSAALVSLALFGAFVSRAF+ ++VL+PKV +GL+VGAMLPYWFSAMTMKS

Sbjct: 546

AAIGKGFAIGSAALVSLALFGAFVSRAGMavinVLSPKVFGVVGAMLPYWFSAMTMKS 605

Query: 601

VGSAALKMVEEVRRQFNTPGLMEGTAKPDYATCVKISTDASIKEIMPGLVMLTPLIV 660

VGSAALKMVEEVRRQF IPGLMEG A PDYA+CV+ISTDAS++EM+PPG LV+L PL+

Sbjct: 606

VGSAALKMVEEVRRQFAAIPGLMEGRATPDYASCVRISTDASLREMMPPGALVLLAPLVA 665

Query: 661

GFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPH 720

G FFGV+TL+G+LAG+LVSGVQ+AISASN+GGAWDNAKKYIEAG S+HAK+LGPKGS+ H

Sbjct: 666

GTFFGVQTLAGLLAGALVSGVQVAISASNNSGGAWDNAKKYIEAGASDHAKALGPKGSDAH 725

Query: 721 KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILFK 768

KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFA HGG++FK

Sbjct: 726 KAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFAAHGGILFK 773



>gi|33465893|gb|AAQ19328.1| H+-pyrophosphatase [Oryza sativa (japonica cultivar-group)]

Length = 773

Score = 991 bits (2561), Expect = 0.0

Identities = 543/768 (70%), Positives = 624/768 (81%), Gaps = 12/768 (1%)

Query: 13 EILVPICAVIGIAFSLFQWYVVSRVKLTS-----DLXXXXXXXXXXXXXXD 60

+ ++P CA +GIAF+++QW +VSRVK++

Sbjct: 6

DAVIPACAAVGIAFAVWQWLLSRVKVSPYSAAAAARNGGAGRAVFRPEGEVDDDDGGC 65

Query: 61

YLIEEEEGVNDQSVVAKCAEIQTASEGATSFLTEYKYXXXXXXXXXXXXXLSGSVEG 120

E +G + +A+CAEIQ+AI GA SFLFT+YKY LGSV

Sbjct: 66

GDDEGADGDGGVAAMARCAEIQSAIRVGANSFLFTQYKYLAFTA VFAVVI FLGSVHR 125

Query: 121

FSTDNKPCTYDTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEAR 180

FST+++PC Y + CKPALA A FSTIAF+LGA TSV SGFLGM+IAT ANARTT+EAR

Sbjct: 126

FSTESQPCQYTRGKACKPALANAVFSTIAFLLGAA TSVASGFLGMRIATAANARTTVEAR 185

Query: 181

KGVGKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEITGYGLGGSS 240

+G+G AF AFRSGAVMGFLA+ GLLVLY+ I VF +YYGDDWEGL+E+ITGYGLGGSS

Sbjct: 186

RGIGPAFAAARSGAVMGFLASLGLLVLYVAIKVFGLYYGDDWEGLYESITGYGLGGSS 245

Query: 241

MALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAPIADNVGDNVGDIAGMGSDF 300

MALFGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAPIADNVGDNVGDIAGMGSDF

Sbjct: 246

MALFGRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAPIADNVGDNVGDIAGMGSDF 305

Query: 301 GSYAEASCAA LVV ASISSFGINHDFTAMCYPLLISSM GILVCLITTLFATDFFEIKLVKE

360

GSYAE++CAAL V SISSFG +H+F A+ YPLLISS G++VCLITTLFATD ++K V

Sbjct: 306 GSYAESTCAA LFVGSISSFGADHNFAAVSYPLLISSAGLIVCLITTLFATDLYRVKTVDG

365

Query: 361

IEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCGWLWAGL 420

+ PALK QL+ISTV+MTVG+ +V++ LP FT+F+FG K VKNW LF CV +GLWAGL

Sbjct: 366

VAPALKLQLLISTVLMVGVLVVTFTALPHEFTMFDFGEVKRVKNWHLFFCVTIGLWAGL 425

Query: 421

IIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXX 480

IGF TEY+TSNAYSPV+DVADSCRTGAATNVIFGLALGYK

Sbjct: 426 AIGFTTEYFTSNAYSPVRDVADSCRTGAATNVIFGLALGYKSVIVPVFAIASIYVSFTL
485

Query: 481

XXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTT 540

+YG+AVAALGMLST+ATGLAIDAYGPISDNAGGIAEMAGMSHRIR+RTDALDAAGNTT

Sbjct: 486

ASIYGVAVAALGMLSTVATGLAIDAYGPISDNAGGIAEMAGMSHRIRQRTDALDAAGNTT 545

Query: 541

AAIGKGFAIGSAALVSLALFGAFVSRAPIHTVDLTPKVIIGLLVGAMLPYWFSAUTMKS 600

AAIGKGFAIGSAALVSLALFGAFVSRAPI++VL+PKV+GL+VGAMLPYWFSAUTMKS

Sbjct: 546

AAIGKGFAIGSAALVSLALFGAFVSRAPIAVINVLSPKVFGVVGAMLPYWFSAUTMKS 605

Query: 601

VGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIV 660

VGSAALKMVEEVRR+F IPGLMEG A PDYA+CV+ISTDAS++EM+PPG LV+L PL+

Sbjct: 606

VGSAALKMVEEVREFAAIPGLMEGRATPDYASCVRISTDASLREMMPPGALVLLAPLVA 665

Query: 661

GFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPH 720

G FFGV+TL+G+LAG+LVSGVQ+AISASN+GGAWDNAKKYIEAG S+HAK+LGPKGS+ H

Sbjct: 666

GTFFGVQTLAGLLAGALVSGVQVAISASNSGGAWDNAKKYIEAGASDHAKALGPKGSDAH 725

Query: 721 KAAVIGDTIGDPLKDTGPSLNILIKLMAVESL VFAPFFATHGGILFK 768

KAAVIGDTIGDPLKDTGPSLNILIKLMAVESL VFAPFFA HGG++FK

Sbjct: 726 KAAVIGDTIGDPLKDTGPSLNILIKLMAVESL VFAPFFAAHGGILFK 773

>gi|4126976|dbj|BAA36841.1| vacuolar H⁺-pyrophosphatase [Chara corallina]

Length = 793

Score = 941 bits (2433), Expect = 0.0

Identities = 510/755 (67%), Positives = 588/755 (77%), Gaps = 14/755 (1%)

Query: 14

ILVPICAVIGIAFSLFQWYWSRVKLTSDLXXXXXXXXXXXXXXDYLIIEEEGVNDQS 73

I +P VIGI F++ QW VV ++ + +Y + +EG+ D S

Sbjct: 41 IFIPAACVIGILFAVLQWSVVGKISVRPS-----GGGMNYPLMGDEGLEDSS 87

Query: 74

VVAKCAEIQTaisegatsflfTEYKYXXXXXXXXXXXXXLSVGSVEGFSTDNKPCYDTT 133

VV +CAEIQ AISEGA SFL TEYKY LG+ E F TD KPC +D T

Sbjct: 88

VVTRCAEIQEAISEGAVSFLMTEYKYLSYFMVGFFIVFAFLGATEDFGTDRKPCEWDAT 147

Query: 134

RTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGVGKAFIVAFRS 193

+ C + A S +AF LGA+TS L GFLGMKIAT+ANART GVG AF AFRS

Sbjct: 148

KLCGSGVMNALLSAVAFALGAITSTLCGFLGMKIATFANARTRSRRGGVGPAFKAAFRS 207

Query: 194

GAVMGFLLAASGLLVLYITINVFKIYYGDDWEGLFEITGYGLGGSSMALFGRVGGIYT 253

GAVMGFL + GL+VLY TI +F+ YYGDDW GL+E+I GYGLGGSS+ALFGRVGGIYT

Sbjct: 208

GAVMGFLLTSGLIVLYFTILIFQRYYGDDWIGLYESIAGYGLGGSSVALFGRVGGIYT 267

Query: 254

KAADVGADELVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAEASCAALVV 313

KAADVGADELVGK+ERNIPEDDPRNPAVIADNVGDNVGDIAGMG+DLFGS AE++CAALVV

Sbjct: 268

KAADVGADELVGKVERNIPEDDPRNPAVIADNVGDNVGDIAGMGADLFGSLAESTCAALVV 327

Query: 314 ASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFE-IKLVKEIEPALKNQLIIS 372
+S+S FG ++ AM +PLLI+ GILVCLITTL ATD + +K IEPALK QL+IS

Sbjct: 328 SSLSDFGKEMNYVAMSFPPLLITGAGILVCLITTLVATDLTSGVSNIKGIEPALKQQQLVIS
387

Query: 373

TVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGLIIGFVTEYYTSN 432
TV+MT IA+++W LP +F I N KWK W +F CV GLWAGL+IG+ TEY+TS+

Sbjct: 388

TVLMTPVIALLAWGCLPDTFEIINGAETKVVKKWYMFFCVACGLWAGLLIGYTTEYFTSH 447

Query: 433

AYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXXXXXXXXMYGVAVAALG 492
++PV+DVADSCRTGAATNVIFGLALGYK MYG+A AALG

Sbjct: 448 QFTPVRDVADSCRTGAATNVIFGLALGYKSIIPILAIATVFSHTLAAMYGIACAALG
507

Query: 493

MLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTAAIGKGFAIGSA 552
MLST++T LAIDAYGPISDNAGGIAEMA M IRE+TDALDAAGNTAAIGKGFAIGSA

Sbjct: 508

MLSTLSTCLAIDAYGPISDNAGGIAEMAEMGPAIREKTDALDAAGNTAAIGKGFAIGSA 567

Query: 553

ALVSLALFGAFVSRAGIHTVDVLTPVIIGLLVGAMLPYWFSAMTMKSVGSAALKMVEEV 612
ALVSLALFGA+++RAGI +VDV+ PK +GL+VGAMLPYWFSAMTMKSVG AAL MVEEV

Sbjct: 568

ALVSLALFGAYINRAGITSVDVILPKEFVGLIVGAMLPYWFSAMTMKSVGKAALAMVEEV 627

Query: 613

RRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIIPPGCLVMLTPLIVGFFFVETLSGV 672
RRQFNTI GLM+GT KPDY CV+ISTDAS++EMIPPGCLVMLTPL+VG G ETL+G+

Sbjct: 628

RRQFNTIAGLMQGTVKPDYKRCVEISTDASLREMIPPGCLVMLTPLVVGGLLGKETLAGI 687

Query: 673

LAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHKAAVIGDTIGDP 732

LAG+LVSGVQIAISASNTGGAWDNAKKYIEAG ++HA++LGPKGS+ HKAAVIGDT+GDP

Sbjct: 688

LAGALVSGVQIAISASNTGGAWDNAKKYIEAGGNDHARTLGPKGSDCHKAAVIGDTVGD 747

Query: 733 LKDTSGPSLNILIKLMAVESLVFAPFFATHGGILF 767

LKDTSGPSLNILIKLMAVESLVFAPFF T+GG+LF

Sbjct: 748 LKDTSGPSLNILIKLMAVESLVFAPFFKTYGGVLF 782

>gi|45267862|gb|AAS55761.1| putative inorganic diphosphatase (EC 3.6.1.1) [Oryza sativa (japonica cultivar-group)]
Length = 770

Score = 937 bits (2422), Expect = 0.0

Identities = 531/769 (69%), Positives = 615/769 (79%), Gaps = 3/769 (0%)

Query: 5 ALLPELWTEILVPICAVIGIAFSLFQWYVVSRVKLTSDLXXXXXXXXXXXXXXDYLIE
64

AL+ + E+L+P+ AVIGI F++ QWY+VSRV +

Sbjct: 2

ALIGTVAAEVLIPAAVIGILFAVLQWYVMVSRAVPPHDGVGGAGKVERESDGDDGDGDG 61

Query: 65 EEEGVND---

QSVVAKCAEIQTaisegatsflfTEYKYXXXXXXXXXXXXXLSVEGF 121

++ + + V A+CAEIQ AIS GATSFL TEYKY LGSV F

Sbjct: 62

VDDEEDGVDYRGVEARCAEIQHAIsvgatsflmteykyLGAFMAAAVIFVSLGSVGRF 121

Query: 122

STDNKPCTYDTRRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEAR 181

ST +PC YD R C+PALA AAF+ AF+LGA TSV+SG+LGM++AT+ANART LEAR+

Sbjct: 122

STSTEPCPYDAARRCRPALANAFTAAFLGATTSSVSGYLGMRVATFANARTALEARR 181

Query: 182

GVGKAFIVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSM 241

G+G+AF VAFRSGA MGFLA+S LLVL+ +N F +YYGDDW GL+EAITGYGLGGSSM

Sbjct: 182

GIGRAFAVAFRSGAACMGFLASSALLVLFAAVNAFGLYYGDDWGGLYEAITGYGLGGSSM 241

Query: 242

ALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAAVNVDNVGDIAGMGSDLFG 301

ALFGRVGGGIYTKAADVGADLVGK+ERNIPEDDPRNPAAVNVDNVGDIAGMGSDLFG

Sbjct: 242

ALFGRVGGGIYTKAADVGADLVGKVERNIPEDDPRNPAAVNVDNVGDIAGMGSDLFG 301

Query: 302 SYAEASCAALVVASISSFGINHDFTAMCYPLLISSMGILVCLITLFAATDFFEIKLVKEI
361

SYAE+SCAAL VASISSFG +HDF AM YPLL+S+ GI+ C TTL ATD E+ E+

Sbjct: 302

SYAESSCAALFVASISSFGADHDFAAMMYPLLVSAAGIVACAATTLVATDAGELGAADEV 361

Query: 362

EPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGLI 421

PALK Q++ISTV+MT +A V+++ LP SFT+F+FG +K+VKNW LF+CV GLWAGL+

Sbjct: 362

APALKRQILISTVLMATAAVAAVTFLSLPRSFTLFDFGERKLVKNWHLFICVSAGLWAGLV 421

Query: 422

IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXX 481

IG+VTEY+TSNAY PVQ VA SCRTGAATNVIFGLA+GYK

Sbjct: 422 IGYVTEYFTSNAYGPVQTVAQSCRTGAATNVIFGLAVGYKSIVPIFAIAGAIYASFRLA
481

Query: 482

XMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTTA 541

MYG+A+AALGMLSTIATGL IDAYGPISDNAGGIAEMAGM R+RERTDALDAAGNTTA

Sbjct: 482

AMYGIALAALGMLSTIATGLTIDAYGPISDNAGGIAEMAGMPRRVRERTDALDAAGNTTA 541

Query: 542

AIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKSV 601

AIGKGFAIGSAALVSLALFGA+VSRAGI TV+V++P+V +GLL GAMLPYWFSAMTM+SV

Sbjct: 542

AIGKGFAIGSAALVSLALFGAYVSRAGIRTNVVSPRVFVGLLAGAMLPYWFSAMTMRDV 601

Query: 602

GSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVG 661

GSAAL+MVEEVRRQF+ IPGL EG A PDYATCV+ISTDAS++EM+ PG LVM +PL+ G

Sbjct: 602

GSAALRMVEEVRRQFDEIPGLAEGLAAPDYATCVRISTDASLREMVAPGALVMASPLVAG 661

Query: 662

FFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHK 721

FGVE L+G+LAG+LVSGVQ+AISASN+GGAWDNAKKYIEAG +E A+SLGPKGSE HK

Sbjct: 662

TLFGVEALAGLLAGALVSGVQVAISASNSGGAWDNAKKYIEAGATEEARSLGPKGSEAHK 721

Query: 722 AAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

AAVIGDTIGDPLKDTGPSLNIL+KLMAVE+LVFAPFFA HGGI+F +

Sbjct: 722 AAVIGDTIGDPLKDTGPSLNILVKLMAVEALVFAPFFAAHGGIVFNHL 770



>gi|2118183|pir||S61425 inorganic diphosphatase (EC 3.6.1.1), H+-translocating (clone TVP17), vacuolar membrane - common tobacco (fragment)

gi|790475|emb|CAA58699.1| inorganic pyrophosphatase [Nicotiana tabacum]

Length = 541

Score = 881 bits (2277), Expect = 0.0

Identities = 479/541 (88%), Positives = 500/541 (92%)

Query: 230

AITGYGLGGSSMALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNV 289

AITGYGLGGSSMALFGRV GGIYTKAADVGADLVGK+ERNIPEDDPRNPAVIADNVGDNV

Sbjct: 1
AITGYGLGGSSMALFGRVAGGIYTKAADVGADLVGKVERNIPEDDPRNPAVIADNVGDNV 60

Query: 290
GDIAGMGSDLFGSYAEASCAALVVASISSFGINHDFTAMCYPLLISSMGILVCLITTLFA 349
GDIAGMGSDLFGSYAE+SCAALVVASISSFG+NH+FTAM YPLL+SS+GILVCL+TTLFA

Sbjct: 61
GDIAGMGSDLFGSYAESSCAALVVASISSFGVNHEFTAMLYPLLVSSVGILVCLLTLFA 120

Query: 350 TDFFEIKLVKEIEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLF
409
TDFFE+K VKEIEPALK QL+IST +MT GIA+V+W+ LP++FTIFNFG QK VK+WQLF

Sbjct: 121 TDFFEVKAVKEIEPALKQQQLVISTALMTDGIAVVTWIALPSTFTIFNFGAQKEVKSWSQLF
180

Query: 410
LCVCVGLWAGLIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXX 469
LCV VGLWAGLIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK

Sbjct: 181 LCVGVGLWAGLIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFA
240

Query: 470
XXXXXXXXXXXXXXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRER 529
MYG+AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRER

Sbjct: 241 IAVSIFVSFSFAAMYGIAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRER
300

Query: 530
TDALDAAGNTAAIGKGFAIGSAALVSLALFGAFVSRAIHTVDVLTPKVIIGLLVGAML 589
TDALDAAGNTAAIGKGFAIGSAALVSLALFGAFVSRAI TVDVLTPKV IGLVGAML

Sbjct: 301 TDALDAAGNTAAIGKGFAIGSAALVSLALFGAFVSRAAISTVDVLTPKFIGLLVGAML
360

Query: 590
PYWFSAMTMKSVGSAALKMVEEVRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPP 649
PYWFSAMTMKSVGSAALKMVEEVRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMI P

Sbjct: 361

PYWFSAMTMKSVGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIAP 420

Query: 650

GCLVMLTPLIVGFFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA 709
G LVMLTPLIVG FGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA

Sbjct: 421

GALVMLTPLIVGILFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA 480

Query: 710

KSLGPKGSEPHKAAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKY 769
++LGPKGS HKAAVIGDT+GDPLKDTGPSLNILIKLMAVESLVFAPFFATHGG+LFK

Sbjct: 481

RTLGPKGSTAHKAAVIGDTVGDPDKDTGPSLNILIKLMAVESLVFAPFFATHGGLLFKL 540

Query: 770 F 770

F

Sbjct: 541 F 541

>gi|14970742|emb|CAC44451.1| proton-translocating inorganic pyrophosphatase
[Chlamydomonas
reinhardtii]
Length = 762

Score = 833 bits (2153), Expect = 0.0

Identities = 481/776 (61%), Positives = 574/776 (73%), Gaps = 33/776 (4%)

Query: 8 PELWTEILVPICAVIGIAFSLFWYVVSRVKLTSDLXXXXXXXXXXXXXXDYLIEEEE
67

P+ +P AV+ I F++F W V+ +++T +YL+EEE+

Sbjct: 4 PDALIAAFIPASAVALFAVFLWKRVAAIQMTG-----GRVLSSQNGREYLLEEEQ 55

Query: 68

GVNDQSVVAKCAEIQTaisegatsflteykyXXXXXXXXXXXXXlgsvegfstdnkp 127

++ +VAK A+IQ +ISEGA+SFL TEY Y L V

Sbjct: 56 RGGEELVAKAADIQKSISSEGASSFLATEYYYLGIFMVIMSVVICSLLSIV----- 106

Query: 128

CTYDTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGVGKAF 187

T + RT L FSTIAF LG TS+LSG+LGM+IAT+ANART +EARKG+ AF

Sbjct: 107 -

TPEEGRTSADELRNGVFSTIAFALGGATSILSGYLGMQIATFANARTAVEARKGIAPAF 165

Query: 188

IVAFRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGLF EA ITGYGLGGSSMALFGRV 247

+ AFRSGAVMGFL+ GLL L++ I +F ++GDDW+GLFEAI GYGLGGSS+ALFGRV

Sbjct: 166 MCAFRSGAVMGFLSGFGNLNLFLAITIFS KFFGDDWKGLFEAI-

GYGLGGSSIALFGRV 224

Query: 248

GGGIYTKAADVGADLVGKIERNIPEDDPRNP AVIADNVGDNVGDIAGMGSDLFGSYAEAS 307

GGGIYTKAADVGADLVGK+E++IPEDDPRNP AVIADNVGDNVGDIAGMG+DLFGS+AE++

Sbjct: 225

GGGIYTKAADVGADLVGKVEKDIPEDDPRNP AVIADNVGDNVGDIAGMGADLFGSFAEST 284

Query: 308 CAALVVASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEIEPALKN

367

CAALV++++SS G HD+ M +PLLIS+ GI VCLITT ATD K++ EIE LK

Sbjct: 285 CAALVISAVSSLGKEHDYAGMMFPLLISATGIFVCLITTFLATDLKPAKVIAEIEHTLM

344

Query: 368 QLIISTVIMT-VGIAIVSWGLPTSFTIFNFGT-----QKVVKNWQLFLCVCVGLWAG

419

QLIIST++MT V + + W LP FT+ + +KVVK+W+F+C+ GLW G

Sbjct: 345 QLIISTLLMTPVALGVALW-

SLPPEFTLSVPSSSPDKPFDEKVVKSWMFVCISTGLWGG 403

Query: 420

LIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXX 479

L++G TEY+TSN Y PVQDVAD+CRTGAAT++IFGLALGYK

Sbjct: 404 LLVGLQTEYFTSNRYKPVQDVADACRTGAATDIIFGLALGYKSCIPTIVGVAIYVGTS
463

Query: 480

XXXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNT 539
M+G+A ALGMLST+ATGLAIDAYGPISDNAGGIAEMAGM IRERTDALDAAGNT

Sbjct: 464

LAGMFGIACCALGMLSTLATGLAIDAYGPISDNAGGIAEMAGMGEDIRERTDALDAAGNT 523

Query: 540 TAAIGKGFAIGSAALVSLALFGAFVSRAGIHTV--DVLTPKVIIGLLVGAMLPYWFSAMT
597

TAAIGKGFAIGSAALVSLALFGA+V+RA I + +L P+V GLL+GAMLPYWFSAMT

Sbjct: 524

TAAIGKGFAIGSAALVSLALFGAYVTRAKIDMIHSSILDPRVFAGLLLGAMLPYWFSAMT 583

Query: 598

MKSVGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTP 657
MKSVG AAL MV EVRRQFNTI GLMEGTA+PDY CV IST A+I EMI PG LV+ TP

Sbjct: 584

MKSVGKAALAMVHEVRRQFNTIAGLMEGTARPDYKRCVAISTQAISEMIAPGALVIFTP 643

Query: 658

LIVGFFFVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGS 717
++VG FG + L+GVLAGSLVSGVQ+A+S NTGGAWDNAKKYIEAG +EHA+ LG KGS

Sbjct: 644

VVVGALFGTQCLAGVLAGSLVSGVQLAVSMSNTGGAWDNAKKYIEAGATEHARELGGKGS 703

Query: 718 EPHKAAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFF--ATHG-GILFKYF 770
+ HKAAVIGDT+GDPLKDT+GPSLNILIKLMAVESLVFAPFF HG G++F +F

Sbjct: 704 DCHKAAVIGDTVGDPDKDTNGPSLNILIKLMAVESLVFAPFFYNCAHGQQGLIFSFF 759



>gi|1049255|gb|AAA80347.1| H+-pyrophosphatase

Length = 509

Score = 815 bits (2106), Expect = 0.0
Identities = 443/507 (87%), Positives = 467/507 (92%)

Query: 225

EGLFEAITGYGLGGSSMALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAAVNADN 284
EGLFEAITGYGLGGSSMALFGR+GGGIYTKAADVGADLVGK+ERNIPEDDPRNPAAVNADN
Sbjct: 1
EGLFEAITGYGLGGSSMALFGRLLGGGIYTKAADVGADLVGKVERNIPEDDPRNPAAVNADN 60

Query: 285

VGDNVGDIAGMGSDLFGSYAEASCAALVVASISSFGINHDFTAMCYPLLISSMGILVCLI 344
VGDNVGDIAGMGSDLFGSYAE+SCAALVVASISSFGINH+FT M YPLL+SS+GI+ CLI
Sbjct: 61 VGDNVGDIAGMGSDLFGSYAESSCAALVVASISSFGINHEFTPWYPLLSSVGIIACLI
120

Query: 345 TTLFATDFFEIKLVKEIEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVK
404

TTLFATDFFEIK V EIEPALK QLIIST++MT+GIA++SW+GLP +FTIFNFG QK V+
Sbjct: 121 TTLFATDFFEIKAVDEIEPALKKQLIISTIVMTIGIALISWLGLPYTFTIFNFGVQKTVQ 180

Query: 405

NWQLFLCVCVGLWAGLIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXX 464
+WQLFLCV VGLWAGL+IGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK
Sbjct: 181
SWQLFLCVAVGLWAGLVIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVI 240

Query: 465

XXXXXXXXXXXXXXXXXXXXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSH 524
MY VAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSH
Sbjct: 241 IPIFAIAFSIFLSFLSLAAMYXVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSH
300

Query: 525 RIRERTDALDAAGNTAAIGKGFAIGSAALVSLALFGAFVSRAIHTVDVLTPKVIIGLL
584

RIRERTDALDAAGNTAAIGKGFAIGSAALVSL LGAFVSRA I TVDVLTPEVFIGLI
Sbjct: 301 RIRERTDALDAAGNTAAIGKGFAIGSAALVSLRLFGAFVSRAAISTVDVLPEVFIGLI
360

Query: 585

VGAMLPYWFSAMTMKSVGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIK 644

VGAMLPYWFSAMTMKS+GSAALKMVEEVRRQFNTIPGLMEGT KPDYATCVKISTDASIK

Sbjct: 361

VGAMLPYWFSAMTMKSMGSAALKMVEEVRRQFNTIPGLMEGTTKPDYATCVKISTDASIK 420

Query: 645

EMIPPGCLVMLTPLIVGFFFVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAG 704

EMIPPG LVMLTPLIVG FGVETLSGVLAG+LVSGVQIAISASNTGGAWDNAKKYIEAG

Sbjct: 421

EMIPPGALVMLTPLIVGILFGVETLSGVLAGALVSGVQIAISASNTGGAWDNAKKYIEAG 480

Query: 705 VSEHAKSLGPKGSEPHKAAVIGDTIGD 731

VSEHA++LGPKGS+PHKAAVIGDTIGD

Sbjct: 481 VSEHARTLGPKGSDPHKAAVIGDTIGD 507



>gi|21654895|gb|AAK95376.1| vacuolar-type proton translocating pyrophosphatase 1

[Trypanosoma

brucei]

Length = 826

Score = 692 bits (1786), Expect = 0.0

Identities = 405/779 (51%), Positives = 515/779 (66%), Gaps = 56/779 (7%)

Query: 15

LVPICAVIGIAFLQWYVSRVKLTSDLXXXXXXXXXXXXXXDYLIIEEEGVNDQSV 74

+++ + G +F+++ WYV S +K+T Y+I +

Sbjct: 79 IIIFLASAFGFAMYWYVASDIKITPGKGNIMRNAHLTDEVMRNYYVISKR----- 130

Query: 75 VAKCAEIQTaisegatsflfTEyKYYYYYYYYYYYYYYLG---SVEGFSTDNKPCTY

130

+S+GA +FLF EY+Y LG S +G D +P

Sbjct: 131 -----VSDGANAFLFAEYRYMGIFMLGFGALLYFLLGVAMSSPQGEGKDGRPPV-
179

Query: 131 DTTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGVGK----
185

+ AAFS AFV+GA TSVL+G++GM+IA Y N+RT + A G G

Sbjct: 180 ---

AVEAPWVNAAFSLYAFVIGAFTSVLAGWIGMRIA VYTN SRTAVMATVGSGGSDNDV 235

Query: 186 -----AFIVAFRSGAVMGFLLAASGLLVLYITINVFKIYYGDDWE---GLFEA 230
AF AFR G MGF L + GL L+ T+ + + Y+GD E LFE

Sbjct: 236

LANGSQSRGYALAFQTAFRGGITMGFALT SIGLFALFCTVKLMQTYFGDSAERLPELFEC 295

Query: 231

ITGYGLGGSSMALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRRNPAVIADNVGDNVG 290
+ +GLGGSS+A FGRVGGGIYTKAADVGADLVGK+E+NIPEDD RNP VIAD +GDNVG

Sbjct: 296

VAAFLGGSVACFGRVGGGIYTKAADVGADLVGKVEKNIPEDDARNPGVIADCIGDNVG 355

Query: 291 DIAGMGSDLFGSYAEASCAALVVASISSFGINHDFTAMCYPLLISSMGILVCLITLFA
350

DIAGMGSDLFGS+ EA+CAALV+A+ SS ++ DFT M YPLLI++ GI VC+ T L A

Sbjct: 356 DIAGMGSDLFGSFGEATCAALVIAA-SSAELSADFTCMMYPLLITAGGIFVCIGTALLAA
414

Query: 351 DFFEIKLVKEIEPALKNQLIISTVIMTVGIAIVSWGLPTSFTIFNFGTQKVVKNWQLFL
410

+K ++IEP LK+QL++ST+ TV+ ++ LP +FT+ TK W+ +

Sbjct: 415 TNSGVKWAEDIEPTLKHQLLVSTIGATVVLVITAYSLPDAFTVGAVETTK---WRAMV
470

Query: 411

CVCVGLWAGLIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXX 470
CV GLW+GL+IG+ TEY+TSN+Y PVQ++A+SC TGAATN+i+GL+LGY

Sbjct: 471 CVLCGLWSGLLIGYSTEYFTSNSYRPVQEIAESCETGAATNIIYGLSLGYISVLPII
530

Query: 471

XXXXXXXXXXXXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERT 530

+YG A+AALG+LST++ L IDAYGPISDNAGGIAEMA M H IRE T

Sbjct: 531 AFTIYLSHHCAGLYGYALAALGILSTMSIALTIDAYGPISDNAGGIAEMAHMGEIREIT
590

Query: 531

DALDAAGNTAAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLP 590

DALDAAGNTAAIGKGFAIGSAA V+LAL+GA+VSR GI TV++L +V+ GLL+GAMLP

Sbjct: 591

DALDAAGNTAAIGKGFAIGSAAFVALALYGAYVSRVGISTVNLLDARVMAGLLLGAMLP 650

Query: 591

YWFSAMTMKSVGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPG 650

YWFSAA+TMKSVG AA+ MV E+RRQF P + GT +PDY +CV I+T A++++M+ P

Sbjct: 651 YWFSALTMKSVGVAAMDMVNEIRRQFQD-

PAVAAGTKEPDYESCVNIATGAALQQMVAPA 709

Query: 651

CLVMLTPLIVGFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAK 710

CLVML P++ G FG TL+G+L G+LVSGVQ+AISASNTGGAWDNAKKYIE G K

Sbjct: 710 CLVMLAPIVTGILFGRYTLAGLLPGALVSGVQVAISASNTGGAWDNAKKYIEKG-
GLRDK 768

Query: 711 SLGPKGSEPHKAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATH-GGILFK

768

S G KGS H AAVIGDT+GDPLKDTSGP+LNIL+KLMA+ S+VFAP + GG+L K

Sbjct: 769 SKG-KGSPQHAAVIGDTVGDPDKDTSGPALNILVKLMAIISVVFAPVVQSKLGGLLVK
826

>gi|8886133|gb|AAF80381.1| vacuolar-type proton translocating pyrophosphatase 1;

PPase1

[Trypanosoma cruzi]

Length = 816

Score = 681 bits (1757), Expect = 0.0

Identities = 399/781 (51%), Positives = 520/781 (66%), Gaps = 48/781 (6%)

Query: 4 PALLPELWTEILVPICAVIGIAFSLFQWYVVSRVKLTSDLXXXXXXXXXXXXDYLI
63

P L+ T +++ A +G +F+++ WYWVS +++T YL

Sbjct: 67 PPLMSADVTTVIIVTSAALGFSFAMYWWYVVSEIRITP-----GKDQGMRNAYLT 116

Query: 64

EEEEGVNDQSVAKCAEIQTaisegatsflfTEYKYXXXXXXXXXXXXXXLGSVEGFST 123
+E V+ I +SEGA +FL+ EY+Y LG +S+

Sbjct: 117 DE-----VMRNVYVISRRVSEGANAFLYAEYRYMGLFMAFGTLIFFLLGV--AYSS 166

Query: 124

DNKPCTYDTTRCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKG- 182
+ +R A AA S +AF +G++TSV +G++GM+IA Y NART + A +G

Sbjct: 167 PQ-----

EGSRPVASPWANAALSLAFFVGSLTSVFAGWIGMRIA VTNARTAVMATEGS 221

Query: 183 -----VGKAFIVA FRSGAVMGFLAASGLLVLYITINVFKIYYGDDWEGL---FEAI 231

KAF AFR G MGF L ++GL L++ + V Y+ D E+ +E+

Sbjct: 222

EEGDQSLGFAKAFQTAFRGGITMGFALT SAGLFLFV PVK VIGAY FDDAPENV LVYECV 281

Query: 232 TGYGLG-

GSSMALFGRVGGGIYTKAADVGADLVGKIERNIPEDDPRNP AVIADNVGDNVG 290
+GL G+++A F RVGGGIYTKAADVGADLVGK+ERNIPEDD RNP VIAD +GDNVG

Sbjct: 282

AAFGLRVGTAVACFARVGGGIYTKAADVGADLVGKVERNIPEDDARNPGVIADCIGDNVG 341

Query: 291 DIAGMGSDLFGSYAEASCAA LVVASISSFGINHDFTAMCYPLLISSMGILVCLITLFAT
350

DIAGMGSDLFGS+ + SCA LV+A+ S ++ +FT M YPLLI+++GILVC+ + L

Sbjct: 342 DIAGMGSDLFGSFGQTSCAELVIAA-GSAELSSEFTYMMYPLLITAVGILVCIGSALIVA
400

Query: 351 DFFEIKLVKEIEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFL
410

+ ++ ++++EP LK QL+ STV TV + ++ GLP +FT+ T K W+ +

Sbjct: 401 NNSGVQRAEDVEPTLKRQLLFSTVAATVALVFLDFGLPDTFTVGTATTK---WRALV
456

Query: 411 CVCVGLWAGLIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGY-
XXXXXXXXXX 469

CV GLW+GLIIG+ TEYYTSNAY PVQ++A++C TGAATN+I+GL+LGY

Sbjct: 457

CVMCGLWSGLIIGYTTEYYTSNAYHPVQEIAEACETGAATNIIYGLSLGYFSVPPILAM 516

Query: 470

XXXXXXXXXXXXXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRER 529
+YG A+AALG+LST++ L IDAYGPISDNAGGIAEMA M H IRE

Sbjct: 517 AVTILSASYRMAADLYGFALAALGILSTMSIALTIDAYGPISDNAGGIAEMAHMHGHEIREI
576

Query: 530

TDALDAAGNTAAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAML 589
TDALDAAGNTAAIGKGFAI SAA V+LAL+ A+VSR GI T+++L +V+ GLLVGAML

Sbjct: 577 TDALDAAGNTAAIGKGFAIASAAFVALALYYAAYSRVGIPTINILDARVMSGLLVGAML
636

Query: 590

PYWFSAMTMKSVGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPP 649

PY FSA TMKSVG AA+ MV E+RRQF P + EGT +PDY +CV I+T A++++M+ P

Sbjct: 637 PYCFSAFTMKSVGLAAMDMVNEIRRQFQN-
PAIAEGTEEPDYESCVAIATQAALQQMVAP 695

Query: 650

GCLVMLTPLIVGFFFVETLSVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHA 709
CLVMLTP++VG FG TL+G+L G++VSGVQ+AISASNTGGAWDNAKKYIE G

Sbjct: 696 ACLVMLTPIVVGVLFGRYTLAGLLPGIAVSGVQVAISASNTGGAWDNAKKYIEKG-
GLRD 754

Query: 710 KSLGPKGSEPHKAAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATH-GGILFK
768

K+ G KGS H AAVIGDT+GDPLKDTSGP+LNILIKLMA+ S+VFAP F + GGI+ +

Sbjct: 755 KNKG-KGSPQHAAVIGDTVGDPLKDTSGPALNILIKLMAISVVFAPVFESQLGGIIMR
813

Query: 769 Y 769

Y

Sbjct: 814 Y 814

□ >gi|24214171|ref|NP_711652.1| Pyrophosphate-energized vacuolar membrane proton pump [Leptospira

interrogans serovar Lai str. 56601]

gi|45658133|ref|YP_002219.1| H+-translocating pyrophosphatase [Leptospira interrogans serovar

Copenhageni str. Fiocruz L1-130]

gi|33301182|sp|Q8F641|HPPA_LEPIN Pyrophosphate-energized proton pump (Pyrophosphate-energized

inorganic pyrophosphatase) (H+-PPase) (Membrane-bound proton-translocating pyrophosphatase)

gi|24195070|gb|AAN48670.1| Pyrophosphate-energized vacuolar membrane proton pump [Leptospira

interrogans serovar lai str. 56601]

gi|45601375|gb|AAS70856.1| H+-translocating pyrophosphatase [Leptospira interrogans serovar

Copenhageni str. Fiocruz L1-130]

Length = 704

Score = 646 bits (1667), Expect = 0.0

Identities = 381/697 (54%), Positives = 483/697 (69%), Gaps = 38/697 (5%)

Query: 77 KCAEIQTAISEGATSFLFTEYKYXXXXXXXXXXXXXXLGS--
VEGFSTDNKPCTYDTTR 134

K EI +AISEGA +FL EYK L + EGF+

Sbjct: 42 KLEIASSAEGAMAFLVREYKVISLFIAMAVLIVLLLDNPGSEGFND----- 90

Query: 135

TCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGVGKAFIVAFRSG 194

++ IAFV GA+ S +SGF+GMKIAT N RT A+ + KAF VAF SG

Sbjct: 91 -----GIYTAIAFVSGALISCISGFIGMKIATAGNVRTAEAAKSSMAKAFRVAFDSG 142

Query: 195 AVMGFLLAASGLLVLYITINVFK-

IYYGDDWEGLFEAITGYGLGGSSMALFGRVGGGIYT 253

AVMGF L +L + + VF +Y G + L E++ G+GLGGS++ALFGRVGGGIYT

Sbjct: 143

AVMGFLVGLAILGMIVLFLVFTGMYPGVEKHFLMESLAGFGLGGSVALFGRVGGGIYT 202

Query: 254

KAADVGADELVGKIERNIPEDDPRNPAPIADNVGDNVGDIAGMGSDLFGSYAEASCAALVV 313

KAADVGADELVGK+E+ IPEDDPRNPAPIADNVGDNVGDIAGMGSDLFGSYAEASCAALVV+

Sbjct: 203

KAADVGADELVGKVEKGIPEDDPRNPATIADNVGDNVGDIAGMGSDLFGSCAEATCAALVI 262

Query: 314 ASISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEIEPALKNQLIIST
373

++S ++ A+ YPLLIS+ GI ++T+ A +K +E ALK QL +ST

Sbjct: 263 GATAS-ALSGSVDALLYPLLISAFGIPASILTSFLA---RVKEDGNVESALKVQLWVST
317

Query: 374

VIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVGLWAGLIIGFVTEYYTSNA 433

+++ + V+ + SF I K + W +++ + VGL++G+ IG VTEYYTS++

Sbjct: 318 LLVAGIMYFVTKTFMVDSFEI---AGKTITKWDVYISMVVGFLSGMFIGIVTEYYTSHS
373

Query: 434

YSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXXMYGVAVAALGM 493

Y PV++VA++ TGAATN+I+GL+LGY MYG+A+AALGM

Sbjct: 374 YKPVREVAEASNTGAATNIIYGLSLGYHSSVIPVILLVITVTANLLAGMYGIAIAALGM
433

Query: 494

LSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRIRERTDALDAAGNTAAIGKGFAIGSAA 553

+STIA GL IDAYGP+SDNAGGIAEMA + +R+RTD LDAAGNTAAIGKGFAIGSAA

Sbjct: 434 ISTIAIGLTIDAYGPVSDNAGGIAEMAELGKEVRDRTDTLDAAGNTAAIGKGFAIGSAA

493

Query: 554

LVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKSVGSAALKMVEEV 613

L SLALF AF++R +++VL +V GL+ GAMPL+ F+AMTMKSVG AA+ MVEEV

Sbjct: 494

LTSLALFAAFITRTHTSLEVLNAEVFGGLMFGAMLPFLFTAMTMKSVGKAADVDMVEEV 553

Query: 614

RQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFFFVETSGVL 673

+QF IPG+MEG KPDY CV IST A+++EMI PG LV+LTP++VG+ FGV+TL+GVL

Sbjct: 554 KQFKEIPGIMEGKNKPDYKRCVDISTSAAALREMILPGLLVLTPILVGYLFGVKTLAGVL

613

Query: 674

AGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHKAAVIGDTIGDPL 733

AG+LV+GV +AISA+N+GG WDNAKKYIE K G KGS+ HKAAV+GDT+GDP

Sbjct: 614 AGALVAGVVLAlisaANSGGGWDNAKKYIE-----KKAGGKGSDQHKAAVVGDTVGDPL

666

Query: 734 KDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770

KDTGPS+NILIKLMA+ SLVFA FF GG++FK F

Sbjct: 667 KDTGPSINILIKLMAITSVFAEFFVQQGGLIFKIF 703

>gi|13661740|gb|AAK38077.1| H+-translocating inorganic pyrophosphatase TVP1
[Toxoplasma gondii]

Length = 816

Score = 611 bits (1576), Expect = e-173

Identities = 375/766 (48%), Positives = 480/766 (62%), Gaps = 61/766 (7%)

Query: 12 TEILVPICAVIGIAFSLFQWYVVSRVKLTSDLXXXXXXXXXXXXXXDYLIEEEGVND
71

T L+ + ++IG+ ++++++ VS++++ L D L E G N

Sbjct: 83 TTCLLLLPSIIGLFWAVYEAWKVSKIQMDGPLGDDNKRLT-----DPLYLEMSG-NI 133

Query: 72

QSVVAKCAEIQTaiseGATsFLFTEYKYXXXXXXXXXXXXXLSVGFSTDNKPCTYD 131

Q + I I++GA +FL E+KY +G

Sbjct: 134 QQQLNMMKSISRCIADGAVTFLTQEFKYMAVYIVVFSSILGIFVGI----- 179

Query: 132

TTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGVGKAFIVAF 191

P+A AFVLGA+TS+L GF+GMKIA Y+N RT EA +G+ F VA

Sbjct: 180 -----PTMA-----AFVLGALTSILCGFVGGMKIAVYSNVRTCHEAWMELGRGFQVAL 226

Query: 192 RSGAVMGFLLAASGLLVLYITINVFKI--YYG---DDWEGLFEAITGYGLGGSSMALFGR
246

+G+VMGF L + G L L I +++++ +G +D LFEA+ GYGLGGSS+ALF R

Sbjct: 227

TAGSVMGFALVSLGCLTLVAIILYRLPSLFGTNPEDQRALFEAVAGYGLGGSSIALFAR 286

Query: 247

VGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAEA 306

VGGGIYTKAADVGADL GK E + EDDPRNPA IADNVGDNVGD+AGMG+DLFGS AEA

Sbjct: 287

VGGGIYTKAADVGADLSGKNEYGMSEDDPRNPACIADNVGDNVGDVAGMGADLFGSLAEA 346

Query: 307 SCAALVVASIS-----SFGINHDFTAMCYPLLISSMGILVCLITLFAFDFFEIKLV 358

SCA LV+A S G+ H + + +P+LISS GI + T + F ++

Sbjct: 347

SCAGLVIAGASIATSASGGPQGLAHWSGLMFPVLISSTGIFTGIFTVVLVRACFSVRCY 406

Query: 359

KEIEPALKNQLIISTVIMTVGIAIVSWGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWA 418

+IE ALK + IST + + ++S+ LP+ F+ G Q W +CV +GLWA

Sbjct: 407 DDIEKALKWWMFISTGLEMPVLILLSYFFLPSEFLLD--
GCQGTTAWWHAACVVLGLWA 464

Query: 419

GLIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXX 478
GL IG+VTEYYTS++Y PV++++ + AAT +I+GLALGY

Sbjct: 465 GLAIGYVTEYYTSHSYFPVREISQTQIVSAATGIIYGLALGYSSTVPIICLGVTILVSH
524

Query: 479

XXXXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGN 538
MYG+A+AALGMLST+ GL ID YGPISDNAGGIAEMAG+ +R RTDALDAAGN

Sbjct: 525

TLCGMYGINALAALGMLSTLTMGLMIDGYGPISDNAGGIAEMAGLGPEVRSRTDALDAAGN 584

Query: 539

TTAAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTM 598
TTAA+GKG+AIGSAALVSLALFGAF RA I VDVL P GLL GAM+PY FSAMTM

Sbjct: 585

TTAAVGKGYAIGSAALVSLALFGAFTVRAHITAVDVLDPWTFGLFGAMMPYAFSAMTM 644

Query: 599

KSVGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEIMPAGCLVMTPL 658
KSVG AA MV+E +QF P +++G +P Y C++IST AS+ EMI PG LV+ P+

Sbjct: 645 KSVGIAASDMVQECLQQF---PLIIQGNIEPQYKRCIEISTRASLHEMIAPGALVICAPV
701

Query: 659 IVGFFFVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGV--
SEHAKSLGPKG 716

G FG +G+LAG+LVSG+Q+AISAS +G AWDNAKKYIE+G ++H KG
Sbjct: 702 AAGMMFGKNCTAGLLAGALVSGIQLAISASTSGSAWDNAKKYIESGALGADHG----
KG 756

Query: 717 SEPHKAavigDTIGDPLKDTGPSLNILIKLMAVESL VFAPFFATH 762

S+ HK AV GDT+GDPLKDTGPSLNILIKL A+ SLVF F A H
Sbjct: 757 SQAHKNAVTDGTVGDPLKDTGPSLNILIKLSAIISLVFGAFIAEH 802

>gi|13661738|gb|AAK38076.1| H+-translocating inorganic pyrophosphatase TVP1
[Toxoplasma gondii]
Length = 816

Score = 610 bits (1573), Expect = e-173

Identities = 376/766 (49%), Positives = 479/766 (62%), Gaps = 61/766 (7%)

Query: 12 TEILVPICAVIGIAFSLFQWYVSRVKLSDLXXXXXXXXXXXXXXDYLIEEEGVND
71

T L+ + ++IG+ +++++ + VS++++ L D L E G N

Sbjct: 83 TTCLLLLPSIIGLFWAVYEAWKVSKIQMDGPLGDDNKRLT-----DPLYLEMSG-NI 133

Query: 72

QSVVAKCAEIQTaisegatsflfTEYKYXXXXXXXXXXXXLGSVEGFSTDNKPCTYD 131

Q + I I++GA +FL E+KY LG G T

Sbjct: 134 QQQLNMMKSISRCIADGAVTFLTQEFKYMAVYIVVFSSI---LGIFVGIRT----- 181

Query: 132

TTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGVGKAFIVAF 191

AFVLGA+TS+L GF+GMKIA Y+N RT EA +G+ F VA

Sbjct: 182 -----MAAFVLGALTSLCGFVGGMKIAVYSNVRTCHEAWMELGRGFQVAL 226

Query: 192 RSGAVMGFLLAASGLLVLYITINVFKI--YYG--DDWEGLFEAITGYGLGGSSMALFGR
246

+G+VMGF L + G L L I +++++ +G +D LFEA+ GYGLGGSS+ALF R

Sbjct: 227

TAGSVMGFALVSLGCLTLVAILLYRLPSLFGTNPEDQRALFEAVAGYGLGGSSIALFAR 286

Query: 247

VGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAEA 306

VGGGIYTKAADVGADL GK E + EDDPRNPA IADNVGDNVGD+AGMG+DLFGS AEA

Sbjct: 287

VGGGIYTKAADVGADLSGKNEYGMSEDDPRNPACIADNVGDNVGDVAGMGADLFGSLAEA 346

Query: 307 SCAALVVASIS-----SFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKLV 358

SCA LV+A S G+ H + + + +P+LISS GI + T + F ++

Sbjct: 347

SCAGLVIAGASIATSASGGPQGLAHSWSGLMFPVLISSTGIFTGIFTVVLVRACFSVRCY 406

Query: 359

KEIEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWA 418

+IE ALK + IST + + +S+ LP+ F + G Q W +CV +GLWA

Sbjct: 407 DDIEKALKWVMFISTGLEMPVLILLSYFFLPSEFLLD--

GCQGTTAWWHAACVVLGLWA 464

Query: 419

GLIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXXXX 478

GL IG+VTEYYTS++Y PV++++ + AAT +I+GLALGY

Sbjct: 465 GLAIGYVTEYYTSHSYFPVREISQTQIVSAATGIYGLALGYSSTVPIICLGVTLVSH
524

Query: 479

XXXXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGN 538

MYG+A+AALGMLST+ GL ID YGPISDNAGGIAEMAG+ +R RTDALDAAGN

Sbjct: 525

TLCGMYGIALAALGMLSTLTMGLMIDGYGPISDNAGGIAEMAGLGPEVRSRTDALDAAGN 584

Query: 539

TTAAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAUTM 598

TTAA+GKG+AIGSAALVSLALFGAF RA I VDVL P GLL GAM+PY FSAMTM

Sbjct: 585

TTAAVGKGYAIGSAALVSLALFGAFTVRAHITAVDVLDPWTFGTLLFGAMMPYAFSAMTM 644

Query: 599

KSVGSAALKMVEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPL 658

KSVG AA MV+E +QF P +++G +P Y C++IST AS+ EMI PG LV+ P+

Sbjct: 645 KSVGIAASDMVQECLQQF---PLIIQGNIEPQYKRCIEISTRASLHEMIAPGALVICAPV
701

Query: 659 IVGFFFVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGV--

SEHAKSLGPKG 716

G FG +G+LAG+LVSG+Q+AISAS +G AWDNAKKYIE+G ++H KG
Sbjct: 702 AAGMMFGKNCTAGLLAGALVSGIQLAISASTSGSAWDNAKKYIESGALGADHG----
KG 756

Query: 717 SEPHKAAVIGDTIGDPLKDTSGPSLNILIKLMAVESL VFAPFFATH 762
S+ HK AV GDT+GDPLKDTSGPSLNILIKL A+ SLVF F A H
Sbjct: 757 SQAHKNAVTDVTGDPKDTSGPSLNILIKLSAISLVFGAFIAEH 802

>gi|23509763|ref|NP_702430.1| V-type H(+) -translocating pyrophosphatase, putative
[Plasmodium
falciparum 3D7]
gi|23497614|gb|AAN37154.1| V-type H(+) -translocating pyrophosphatase, putative
[Plasmodium
falciparum 3D7]
Length = 717

Score = 585 bits (1507), Expect = e-165
Identities = 346/696 (49%), Positives = 450/696 (64%), Gaps = 47/696 (6%)

Query: 75
VAKCAEIQTAISEGATSFLFTEYKYXXXXXXXXXXXXXXLGSVEGFSTDNKPCTYDTTR 134
V K EI + I+ GA +FL E++Y + S
Sbjct: 48 VEKMKEIASYIAVGANAFLKKEFQYLAVFIIVFSILLGFFVNS----- 90

Query: 135
TCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGVGKAFIVAFRSG 194
F+ ++FVLG +TS+L G+++GMKIA YAN RTT E K+ K F V +G
Sbjct: 91 -----FTAVSFVLGCLTSILCGYIGMKIAVYANVRTTNETWKS LDKGQVTLNAG 140

Query: 195 AVMGFLLAASGLLVLYITINVFKIYYGDDW---
EGLFEAITGYGLGGSSMALFGRVGGGI 251
VMGF L + G++ L + I V+K Y + + + + I G+GLGGSS+ALF RVGGGI
Sbjct: 141 TVMGFSLVSFGIIALGLLIFVYKTYVFKNTPDNQIYKIIAGFGLGGSSIALFSRVGGGI
200

Query: 252

YTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAEASCAAL 311

YTKAADVGADL GK E IPEDD RNPA IADNVGDNVGD+AGMG+DLFGS AE+ CAAL

Sbjct: 201

YTKAADVGADLSGKNEYGIPEDDIRNPACIADNVGDNVGDMAGMGADLFGSLAESLCAAL 260

Query: 312 VVAS---ISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKLVKEIEPALKN 367

V+ S | + F + +PLL S ++ +IT T + I K++E +LK

Sbjct: 261 VIGSSVISIGEGSPGNAFHCILFPLLVSFSVICSIMTFYIITYSVKINDKKDVEKSLKY

320

Query: 368 QLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGLIIGFVTE

427

L++STV+ ++ | + +V P+ + + K+ W++ + VGLW+GLIIGF TE

Sbjct: 321 LLLLSTVLQSLAILAIGYVCFPS--LVKYNYLKDIHRWKIIVPALVGLWSGLIIGFTTE 377

Query: 428

YYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXXMYGVA 487

+YTS ++SPVQ++A + + AAT +I+GL+LGYK +YG+A

Sbjct: 378 FYTSYSFSPVQEIAHTQKVSATGIIYGLSLGYKSTFIPIICLSATLGISYGLCDIYGIA

437

Query: 488

VAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERTDALDAAGNTAAIGKGF 547

+AA+GMLST+ L IDAYGPISDNAGGIAEMAG+ +RERTD LDAAGNTAAIGKGF

Sbjct: 438 LAAVGMLSTLCICLTIDAYGPISDNAGGIAEMAGLPSEVRERTDILDAAGNTAAIGKGF

497

Query: 548

AIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKSVGSAALK 607

AIGSAALV+ ALFGA+ S A + V++L VIIGLL+GAMLPY FSA+TMKSV AA

Sbjct: 498 AIGSAALVAFAALFGAYASSANLRHVNILNSWVIIGLLIGAMLPLYLFSALTMKSVAIAANS

557

Query: 608

MVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEIMPGLVMLTPLIVGFFFGVE 667

++ E QF P ++EG KPDY C+KISTDAS+++MI PG + + +PLI+G G
Sbjct: 558 VLNECLEQF--PLILEGKQKPDYEKCICIKISTDASLRQMIVPGLISVFSPLIIGMLMGKY
614

Query: 668 TLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGV--
SEHAKSLGPKGSEPHKAAVI 725
+G+L G ++SG+Q+A S++N+GGAWDNAKKYIE+G EH KGS HK +VI

Sbjct: 615 ATAGLLIGIILSGIQLAFSSTNSGGAWDNAKKYIESGALGKEHC----KGSNAHKNSVI
669

Query: 726 GDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFAT 761
GDT+GDPLKDTGPSLNILIKL A+ SLVFA AT
Sbjct: 670 GDTVGDPLKDTGPSLNILIKLSAITSLVFANVIAT 705

>gi|4324984|gb|AAD17215.1| proton-pumping vacuolar pyrophosphatase; plant vacuolar pyrophosphatase homolog; PVP [Plasmodium falciparum]
Length = 717

Score = 585 bits (1507), Expect = e-165
Identities = 346/696 (49%), Positives = 450/696 (64%), Gaps = 47/696 (6%)

Query: 75
VAKCAEIQTASEGATSFLFTEYKYXXXXXXXXXXXXXXLGSVEGFSTDNKPCTYDTTR 134
V K EI + I+ GA +FL E++Y + S
Sbjct: 48 VEKMKEIASYIAVGANAFLKKEFQYLAVFIIVFSILLGFFVNS----- 90

Query: 135
TCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGVGKAFIVAFRSG 194
F+ ++FVLG +TS+L G+++GMKIA YAN RTT E K + K F V +G
Sbjct: 91 -----FTAVSFVLGCLTSILCGYIGMKIAVYANVRTTNETWKS LDKGFQVTLNAG 140

Query: 195 AVMGFLLAASGLLVLYITINVFKIYYGDDW--
EGLFEAITGYGLGGSSMALFGRVGGGI 251
VMGF L + G++ L + I V+K Y + + + I G+GLGGSS+ALF RVGGGI

Sbjct: 141 TVMGFSLVSGIIALGLIFVYKTYVFKNTPDNQIYKIIAGFGLGGSSIALFSRVGGI
200

Query: 252

YTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAEASCAAL 311

YTKAADVGADL GK E IPEDD RNPA IADNVGDNVGD+AGMG+DLFGS AE+ CAAL

Sbjct: 201

YTKAADVGADLSGKNEYGIPEDDIRNPACIADNVGDNVGDMAGMGADLFGSLAESLCAAL 260

Query: 312 VVAS---ISSFGINHDFTAMCYPLLISSMGILVCLITLFATDFFEIKLVKEIEPALKN 367

V+ S I + F + +PLL S ++ +IT T + I K++E +LK

Sbjct: 261 VIGSSVISIGEGSPGNAFHCILFPLLFSFSVICSMITFYIITYSVKINDKKDVEKSLKY

320

Query: 368 QLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCGWLWAGLIIGFVTE
427

L++STV+ ++ | + +V P+ + + K + W++ + VGLW+GLIIGF TE

Sbjct: 321 LLLLSTVLQSLAILAIGYVCFPS---LVKYNYLKDIHRWKIIVPALVGLWSGLIIGFTTE 377

Query: 428

YYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXXMYGVA 487

+YTS ++SPVQ++A ++ AAT +I+GL+LGYK +YG+A

Sbjct: 378 FYTSYSFSPVQEIAHTQKVSAATGIIYGLSLGYKSTFIPICLISATLGISYGLCDIYGIA

437

Query: 488

VAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHIRERERTDALDAAGNTAAIGKGF 547

+AA+GMLST+ L IDAYGPISDNAGGIAEMAG+ +RERTD LDAAGNTAAIGKGF

Sbjct: 438 LAAVGMLSTLCICLTIDAYGPISDNAGGIAEMAGLPSEVRERTDILDAAGNTAAIGKGF

497

Query: 548

AIGSAALVSLALFGAFVSRAGIHTVDLTPKVIIGLLVGAMLPYWFSAUTMKSVGSAALK 607

AIGSAALV+ ALFGA+ S A + V++L VIIGLL+GAMLPY FSA+TMKSV AA

Sbjct: 498 AIGSAALVAFAFGAYASSANLRHVNILNSWVIIGLLIGAMLPYLFALTMKSVIAANS

557

Query: 608

MVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVMLTPLIVGFFFVGE 667

++ E QF P ++EG KPDY C+KISTDAS+++MI PG + + +PLI+G G

Sbjct: 558 VLNECLEQF---PLILEGKQKPDYEKCICIKISTDASLRQMIVPGLISVFSPLIIGMLMGKY

614

Query: 668 TLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGV--

SEHAKSLGPKGSEPHKAASI 725

+G+L G ++SG+Q+A S++N+GGAWDNAKKYIE+G EH KGS HK +VI

Sbjct: 615 ATAGLLIGIILSGIQLAFSSTNSGGAWDNAKKYIESGALGKEHC----KGSNAHKNSVI

669

Query: 726 GDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFAT 761

GDT+GDPLKDTGPSLNILIKL A+ SLVFA AT

Sbjct: 670 GDTVGDPLKDTGPSLNILIKLSAITSLVFANVIAT 705



>gi|23483521|gb|EAA19163.1| V-type H(+) -translocating pyrophosphatase [Plasmodium yoelii]
yoelii]
Length = 716

Score = 582 bits (1501), Expect = e-165

Identities = 356/767 (46%), Positives = 471/767 (61%), Gaps = 73/767 (9%)

Query: 7 LPELWTEILVPICAVIGIAFSLFQWYVVSRVKLSDLXXXXXXXXXXXXXXDYLIEEE

66

+ EL+ I P V+G+ FS+ + +SR+ ++ D L + E

Sbjct: 1 MKELYCIIFGP--PVLGLLFSVIECISISRIHIGAS-----DDKLDKVE 42

Query: 67

EGVNDQSVVAKCAEIQTASEGAT\$FLTEYKYXXXXXXXXXXXXXLSVEGFSTDNK 126

G Q+ + K EI + ISEGASFL EY+Y +

Sbjct: 43 NG---QAKIEKMKEIASYISEGANFLSKEYQYLIVFMILFSGLLSWFINY----- 90

Query: 127

PCTYDTRTCKPALATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGVGKA 186
++ I+F +G +TS++ G++GMKIA YAN RTT E K + K

Sbjct: 91 -----YTAISFAIGCITSIICGYIGMKIAVYANVRTTSETWKSLSDKG 132

Query: 187 FIVAFRSGAVMGFLAASGLLVLYITINVFKIYYG-
DDWEGLF EA ITGYGLGGSSMALFG 245

F V +G VMGF L + ++ L I +K + D L++AI G+GLGGSS+ALF

Sbjct: 133 FKVTLNAGTVMGFSLVSLSIISLGALIFAYKAQFQFSDDPALYKAIAGFGLGGSSIALFS
192

Query: 246

RVGGGIYTKAADVGADLVGKIERNIPEDDPRNPAVIADNVGDNVDIAGMGSDFGSYAE 305
RVGGGIYTKAADVGADL GK E IPEDD RNPA IADNVGDNVGD+AGMG+DLFGS AE

Sbjct: 193

RVGGGIYTKAADVGADLSGKNEYGIPEDDIRNPACIADNVGDNVGD MAGMGADLFGSLAE 252

Query: 306 ASCAALVVAS-----ISSFGINHDFTAMCYPLLISSMGILVCLITTLFATDFFEIKL 357
+ CA+LV+ S + SF IN+ F +PL SS I+ ++T T +

Sbjct: 253 SLCASLVIGSSVSLPENMKSFDINYCFM--FPLFFSSASIISMLTFFLVTKIVRTG
309

Query: 358

VKEIEPALKNQLIISTVIMTVGIAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCGWLW 417
+ +E LK L IST+ ++ I +V LP + + K + NW++ + VGLW

Sbjct: 310 KEGVERTLKYLIFISTIFQSLTIFVVGQYCLPP--VLVYDVLKQIPNWKIIVPALVGLW
366

Query: 418

AGLIIGFTTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXX 477
+GLIIGF TE+YTS ++ PVQ++A++ + AAT +I+GL+LGYK

Sbjct: 367 SG LIIGFTTEFYTSYSFRPVQEIANTQKISAATGIIYGLSLGYKSTFIPICLSGALGIS 426

Query: 478

XXXXXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAG 537
+YGVA+AA+GMLST+ L IDAYGPISDNAGGIAEMAG+ +RE+TD LDAAG

Sbjct: 427

YVFCEVYGVALAAVGMLSTLCICLTIDAYGPISDNAGGIAEMAGLPSEVREKTDILDAAG 486

Query: 538

NTTAAIGKGFAIGSAALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAML PYWFSAMT 597

NTTAAIGKGFAIGSAALV+ ALFGA+ S A + V++L P VIIGLL+G+MLPY FSA+T

Sbjct: 487 NTTAAIGKGFAIGSAALVAFALFGAYASSAKVRHVNILNPWVIIGLLIGSMLPYLFSALT
546

Query: 598

MKSVGSAALKMVEEVRRQFNTIPGLMEGTAKPDYATCVKISTDASI KEMIPPGCLVMLTP 657

MKSV AA ++ E QF P ++ KPDY C+KISTDAS+++MI PG ++ P

Sbjct: 547 MKSVAIAANSVLNECLEQF---PLILANKQKPDYDKCIKISTDASLRQMILPGLISVTFP
603

Query: 658 LIVGFFFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGV--

SEHAKSLGPK 715

LI+G G +G+L G ++SG+Q+A S++N+GGAWDNAKKYIE+G ++H K

Sbjct: 604 LIIGMILMGKYATAGLLIGIILSGIQLAFSSTNSGGAWDNAKKYIESGALGTDHC----K
658

Query: 716 GSEPHKAAVIGDTIGDPLKDTSGPSLNILIKLMAVESLVFAPFFATH 762

GS HK +VIGDT+GDPLKDTSGPS+NILIKL A+ SLVFA + H

Sbjct: 659 GSNAHKNSVIGDTVGDPLKDTSGPSINILIKLSAITSLVFAGLISNH 705

>gi|14149007|emb|CAC39165.1| vacuolar-type H+-pyrophosphatase [Lycopersicon esculentum]

Length = 356

Score = 570 bits (1468), Expect = e-161

Identities = 317/356 (89%), Positives = 323/356 (90%)

Query: 415

GLWAGLIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKXXXXXXXXXXXX 474

GLWAGLIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYK
Sbjct: 1 GLWAGLIIGFVTEYYTSNAYSPVQDVADSCRTGAATNVIFGLALGYKSVIPIFAIASI 60

Query: 475
XXXXXXXXMYGVAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALD 534
MYG+AVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALD
Sbjct: 61
FVSFSFAAMYGIAVAALGMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALD 120

Query: 535
AAGNTTAAIGKGFAIGSAALVSLALFGAFVSRAI TTVLTPKVIIGLLVGAMLPYWFS 594
AAGNTTAAIGKGFAIGSAALVSLALFGAFVSRAI TVDVLTPKV IGLVGAMLPYWFS
Sbjct: 121
AAGNTTAAIGKGFAIGSAALVSLALFGAFVSRAISTVDVLTPKVFIGLLVGAMLPYWFS 180

Query: 595
AMTMKSVGSAALKMVEEVRRQFNTPGLMEGTAKPDYATCVKISTDASIKEMIPPGCLVM 654
AMTMKSVGSAALKMVEEVR QFNTPGLME TAKPDYATCVKI TDASIKEMIPPG LVM
Sbjct: 181
AMTMKSVGSAALKMVEEVRXQFNTPGLMERTAKPDYATCVKIFTDASIKEMIPPGALVM 240

Query: 655
LTPLIVGFFFVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGP 714
LTPLIVG FGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAG SEHA++LGP
Sbjct: 241
LTPLIVGILFGVETLSGVLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGASEHARTLGP 300

Query: 715 KGSEPHKAAVIGDTIGDPLKDTGPSLNILIKLMAVESLVFAPFFATHGGILFKYF 770
KGS+ HKAAVIGDT+GDPLKDTGPSLNILIKLMAVESLVFAPFFATHGG+LFK F
Sbjct: 301 KGSDAHKAAVIGDTVGDPDKDTGPSLNILIKLMAVESLVFAPFFATHGGLLFKL 356

>gi|28210139|ref|NP_781083.1| vacuolar-type H+-pyrophosphatase [Clostridium tetani E88]
gi|33301168|sp|Q898Q9|HPPA_CLOTE Pyrophosphate-energized proton pump
(Pyrophosphate-energized

inorganic pyrophosphatase) (H+-PPase) (Membrane-bound
proton-translocating pyrophosphatase)

gi|28202575|gb|AAO35020.1| vacuolar-type H+-pyrophosphatase [Clostridium tetani E88]

Length = 673

Score = 513 bits (1320), Expect = e-144

Identities = 334/696 (47%), Positives = 426/696 (61%), Gaps = 72/696 (10%)

Query: 80

EIQTAISEGATSFLFTEYKYXXXXXXXXXXXXXXLGSVEGFSTDNKPCTYDTRRTCKPA 139

EI I +GA +FL TEYKY +G

Sbjct: 38 EIAGHIHDGAMAFLKTEYKYLTGFIVIVTVILAIFVG----- 74

Query: 140

LATAAFSTIAFVLGAVTSVLSGFLGMKIATYANARTTLEARKGVGKAFIVAFRSGAVMGF 199

TAA F+LGA+ S+ +G+ GM +AT AN RT AR GKA +AF GAVMG

Sbjct: 75 WQTAACFILGAIFSIFAGYFGMNVATKANVRTAEAARHSQGKALNIAFSGGAVMG

130

Query: 200

LLAASGLLVLYITINVFKIYYGDDWEGLFEAITGYGLGGSSMALFGRVGGGIYTKAADVG 259

+ G++ + I +F G E +TG+GLG SS+ALF RVGGGIYTKAADVG

Sbjct: 131 SVVGLGVVGIGIMYYIFG-----GNMEFVTGFLGASSIALFARVGGGIYTKAADVG

182

Query: 260

ADLVGKIERNIPEDDPRNPAVIADNVGDNVGDIAGMGSDLFGSYAEASCAALVVASISSL 319

ADLVGK+E IPEDDPRNPAVIADNVGDNVGD+AGMG+DLF SY + +AL + ++

Sbjct: 183 ADLVGKVEAGIPEDDPRNPAVIADNVGDNVGDVAGMGADLFESYVGSIIISALTLGTV-

- 239

Query: 320 GINHDFTAMCYPLLISSMGILVCLITLFAATDFFEIKLVKEIEPALKNQLIISTVIMTVG

379

+ + + +PL++SS+GI+ +I LF+ K+ + AL I +I+ V

Sbjct: 240 -VYANKEGVMPLILSSIGIVASIIGILFSRK---SKAKDPQKALNTGTYIGGIIVVS 294

Query: 380

IAIVSWVGLPTSFTIFNFGTQKVVKNWQLFLCVCVGLWAGLIIGFVTEYYTSAYSPVQD 439

AI+S TIF N + F V GL G+IIG +TE YTS+AYS VQ

Sbjct: 295 AAIALS-----NTIFG-----NLKAFFAVASGLVVGMIIGKITEMYTSDAYSSVQK 339

Query: 440 VADSCRTGAATNVIFGLALGYXXXXXXXXXXXXXXXXXXXX-----MYGVAVAAL

491

+A+ TG AT +I GLA+G +YG+++AA+

Sbjct: 340 IANQSETGPATTIISGLAVGMYSTLWPIVLISIGVLVSFFVMGGGSNAMVGLYGISLAAV

399

Query: 492

GMLSTIATGLAIDAYGPISDNAGGIAEMAGMSHRIRERTDALDAAGNTAAIGKGFAIGS 551

GMLST +A+DAYGPI+DNAGGIAEM+ + H +RE TD LD+ GNTAAIGKGFAIGS

Sbjct: 400

GMLSTTGLTVAVDAYGPIADNAGGIAEMSELPEHVREITDKLDVGNTAAIGKGFAIGS 459

Query: 552

AALVSLALFGAFVSRAGIHTVDVLTPKVIIGLLVGAMLPYWFSAMTMKSVGSAALKMVEE 611

AAL +L+LF ++ + ++D+L ++GL +GAMLP+ F A+TM+SVG AA +M+EE

Sbjct: 460 AALTALSLFASYAQATELESIDILNTLVGLFIGAMLPFLFGALTMESVGKAANEMIEE
519

Query: 612

VRRQFNTIPGLMEGTAKPDYATCVKISTDASIKEIMPAGCLVMLTPLIVGFFFFVETLSG 671

VRRQF TIPG+MEG A PDY CV IST A+i+EMI PG L ++ P+ +G G E L G

Sbjct: 520

VRRQFKTIPGIMEGKATPDYKKCVDISTAAIREMILPGVLAIVVPMAMGLLGKEALGG 579

Query: 672

VLAGSLVSGVQIAISASNTGGAWDNAKKYIEAGVSEHAKSLGPKGSEPHKAAVIGDTIGD 731

+LAG+LVSGV +I SN GGAWDNAKKYIE G G KGSE HKAAV+GDT+GD

Sbjct: 580 LLAGALVSGVLVGILMSNAGGAWDNAKKYIEGGAH-----

GGKGSEAHKAAVVGDTVGD 633

Query: 732 PLKDTSGPSLNILIKLMAVESLVFAPFFATHGGILF 767

P KDTSGPS+NILIKLM + SLVFAP +GGIL

Sbjct: 634 PFKDTSGPSMNILIKLMTIVSLVFAPVVLQYGGILL 669

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Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF excluding environmental samples

Posted date: Jun 21, 2004 12:17 AM

Number of letters in database: 619,299,334

Number of sequences in database: 1,865,463

Lambda K H
0.322 0.138 0.405

Gapped

Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 166,000,056

Number of Sequences: 1865463

Number of extensions: 6612265

Number of successful extensions: 18550

Number of sequences better than 10.0: 41

Number of HSP's better than 10.0 without gapping: 34

Number of HSP's successfully gapped in prelim test: 7

Number of HSP's that attempted gapping in prelim test: 18354

Number of HSP's gapped (non-prelim): 60

length of query: 770

length of database: 619,299,334

effective HSP length: 133

effective length of query: 637

effective length of database: 371,192,755

effective search space: 236449784935

effective search space used: 236449784935

T: 11

A: 40

X1: 16 (7.4 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.9 bits)

S2: 78 (34.7 bits)

EXHIBIT B



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Minireview

H⁺-proton-pumping inorganic pyrophosphatase: a tightly membrane-bound family

6352

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Abstract The earliest known H^+ -proton-pumping inorganic pyrophosphatase, the integrally membrane-bound H^+ -proton-pumping inorganic pyrophosphate synthase from *Rhodospirillum rubrum*, is still the only alternative to H^+ -ATP synthase in biological electron transport phosphorylation. Cloning of several higher plant vacuolar H^+ -proto-pumping inorganic pyrophosphatase genes has led to the recognition that the corresponding proteins form a family of extremely similar proton-pumping enzymes. The bacterial H^+ -proton-pumping inorganic pyrophosphate synthase and two algal vacuolar H^+ -proton-pumping inorganic pyrophosphatases are homologous with this family, as deduced from their cloned genes. The prokaryotic and algal homologues differ more than the H^+ -proton-pumping inorganic pyrophosphatases from higher plants, facilitating recognition of functionally significant entities. Primary structures of H^+ -proton-pumping inorganic pyrophosphatases are reviewed and compared with H^+ -ATPases and soluble proton-pumping inorganic pyrophosphatases.

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Key words: H⁺-proton-pumping inorganic pyrophosphatase; H⁺-proton-pumping inorganic pyrophosphate synthase; H⁺-ATPase; H⁺-ATP synthase; Amino acid sequence; Evolution; Enzyme family

1. Introduction

Photophosphorylation of inorganic orthophosphate (Pi) to pyrophosphate (PPi), in chromatophores isolated from the photosynthetic, purple, non-sulfur bacterium *Rhodospirillum rubrum*, was discovered in 1966 [1] and found to be sensitive to uncouplers but uninhibited by oligomycin [2]. This light-induced formation of PPi, which provided a *raison d'être* for the tightly membrane-bound uncoupler stimulated, inorganic pyrophosphatase (PPase) activity in chromatophores [3,4], is still the only known alternative to ATP formation in biological electron transport phosphorylation. In isolated chromatophores, PPi was used to drive several energy requiring reactions [5-8]. Proton movement, which was induced by light in chromatophores [9], was shown by addition of PPi in the dark to be linked also to the PPase [10], thus showing it to be a

H^+ -PPase (H^+ -PPi synthase, compare H^+ -F₀F₁ATPase, H^+ -F₀F₁ATP synthase).

A membrane-bound PPase activity was found in 1975 in homogenates from higher plants [11] and was later localized to plant vacuoles [12]. In plants, the vacuoles contain two enzymes for acidifying the interior of the vacuole, the well known V-ATPase and the V-PPase (V for vacuolar).

Nine amino acid sequences of plant V-PPases have been solved and shown to form a distinct protein family [13-21]. Two are from green algae and have been published very recently [20,21]. The higher plant sequences show identities of more than 85% [18]. From bacteria, the *R. rubrum* H⁺-PPase (PPi synthase) sequence [22] belongs to the same family, as do two homologues which have emerged from genomic work with hyperthermophiles, namely the archaeon *Pyrococcus aerophilum* and the bacterium *Thermotoga maritima*.

H₂-PPase activity has also been documented in several other membranes from higher plants [23-25], as well as in acidocalcisomes from the protozoan *Trypanosoma cruzi* [26] and the cell membrane of the chemotrophic anaerobic bacterium *Syntrophus gentianae* [27].

An excellent review [28] on pyrophosphate as an energy donor in plant cells discusses in great detail the possible interplay between ATP-linked and PP_i-linked reactions. As several recent review articles [29-31] cover the eukaryotic H⁺-PPases, this minireview is somewhat focussed on the prokaryotic homologues. Emphasis is also on H⁺-PPases with a known primary structure and on comparison with both H⁺-ATPases and soluble PPases. X-ray structures at high resolution of crystals from soluble PPases from both pro- and eukaryotes have provided the background for most of the detailed knowledge about the structure and reaction mechanism, also in other PPases. Whereas the membrane-bound PPases are directly involved in bioenergetic reactions, soluble PPases have long been recognized to function in the hydrolysis of the PP_i emerging as a byproduct from various ATP requiring biosyn-

Fig. 1. The first 319 nucleotides from the N-terminal end of the clone RrPP4. The two identical Shine Dalgarno regions (GGAG) and the two possible start codons (ATG and CTG, in bold script) are underlined. Corresponding amino acids for the two alternatives are given.

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Abbreviations: PPI, inorganic pyrophosphate; PPase, inorganic pyrophosphatase; ATP, adenosine triphosphate; ATPase, adenosine triphosphatase

R. rubrum	G G I L T H C A D V G A D L V G - - -
T. maritima	G G G V Y P K A A D M A A D L V G - - -
P. aerophilum	G G G I Y P K A A D L G A D L V G - - -
C. corallina	G G G I Y P K A A D V G A D L V G - - -
A. acetabulum	G G G I Y P K A A D V A A D L V G - - -
O. sativa	G G G I Y P K A A D V C A D L V G - - -
B. vulgaris	G G G I Y P K A A D V G A D L V G - - -
N. tabacum	G G G I Y P K A A D V G A D L V G - - -
C. moschata	G G G I Y P K A A D V G A D L V G - - -
V. radiata	G G G I Y P K A A D V G A D L V G - - -
H. vulgare	G G G I Y P K A A D V G A D L V G - - -
A. thaliana	G G G I Y P K A A D V G A D L V G - - -
consensus	G G G I Y P K A A D V G A D L V G - - -

R. rubrum	G G G A W D N A K K Y I E D G - - - - -
T. maritima	S G C A W D N A K K Y I E D G - - - - -
P. aerophilum	S G C A W D N A K K Y I E D G - - - - -
C. corallina	A G G A W D N A K K Y I E D G - - - - -
A. acetabulum	T G G A W D N A K K Y I E D G - - - - -
O. sativa	S C G A W D N A K K Y I E D G - - - - -
B. vulgaris	T C G A W D N A K K Y I E D G - - - - -
N. tabacum	T O G A W D N A K K Y I E D G - - - - -
C. moschata	T O G A W D N A K K Y I E D G - - - - -
V. radiata	H T C A W D N A K K Y I E D G - - - - -
H. vulgare	T G C A W D N A K K Y I E D G - - - - -
A. thaliana	T G C A W D N A K K Y I E D G - - - - -
consensus	G A W D N A K K Y I E D G - - - - -

Fig. 3. Alignment with the parts of two loops between transmembrane segment 5-6 (above) and 15-16 (below) in H^+ -PPases, where the part of loop 5-6 contains the three motifs GGG, DVGADLVGK and DNVGDNVGD. Residues in black/gray boxes are identical/similar in all sequences. The consensus of similarities follows that of the first organism.

exception is the motif DX₇₋₈KXE [44] in the loop after transmembrane segment 5 which is similar to the active site motif EX₇₋₈KXE in soluble PPases [50]. Antibodies directed to this motif in *V. radiata* V-PPase were recently shown to strongly inhibit the hydrolytic and proton-pumping activity of membrane vesicles and the hydrolytic activity of the purified enzyme [51]. A specific chemical inhibitor for H^+ -PPases from both plants and photobacteria is aminomethylendiphosphonate [52].

Amino acid sequences of algal V-PPases from *Acetabularia acetabulum* [20] and *Chara corallina* [21] have very recently emerged. The *A. acetabulum* sequence shows approximately as many identities with the *R. rubrum* sequence as with the one from *A. thaliana* (see Fig. 2), whereas the *C. corallina* sequence is much more like that of *A. thaliana*. A possible link between vacuolar and bacterial H^+ -PPases is the new homologue from *A. thaliana*. It shows more sequence identities with the *R. rubrum* H^+ -PPase (40.1%) than with any of the vacuolar H^+ -PPases (33.4–37.2%). Furthermore, the homologue contains one of two cysteines of the putative active site loop of the *R. rubrum* H^+ -PPase. The substitution of E in the motif EYYT to K indicates that the homologue may no longer possess coupling activity.

4. Some further structural and evolutionary aspects

The amino acid sequences of the bacterial PPi synthase from *Rhodospirillum*, the homologue from *Thierniota* and nine published vacuolar H^+ -PPases are shown in Fig. 2. Comparisons with hydrophobic plots show that identical (blackened) and similar (shadowed) residues are particularly abundant between transmembrane segments, in the loops 5, 11 and 15.

The homology between all membrane-bound H^+ -PPases has led to various questions, about common structural properties of functional significance and about evolution, both within these archaeal, bacterial, algal and higher plant en-

zymes and between this protein family and possibly related families, such as membrane-bound ATPases and soluble PPases.

4.1. Within the H^+ -PPase family

Attention is here first restricted to corresponding parts of two loops in the PPi synthase from *R. rubrum*. A 45 amino acid piece from the 57 amino acids in the putative active site loop 5 is compared with a similar part of loop 15, which may contain a duplicated and subsequently evolved segment of an ancestral version of loop 5. Three motifs of loop 5 are GGG, DVGADLVGK and DNVGDNVGD.

The first motif, the triglycyl sequence, occurs in all H^+ -PPase family members and may be expected to have the potential to provide, to the extent that other structural properties of the enzyme allow, an unusually high local conformational change capability. In the PPi synthase, uniquely, the loop 15, with the 'duplicated segment', contains a similarly positioned sequence of three glycolyl residues, in contrast to just two or one in all other known H^+ -PPases (Fig. 3). In view of the conformational change mechanism of the ATP synthase function [53,54], one may ask the question if the fact that only the PPi synthase of the H^+ -PPase family may function physiologically in the PPi synthesis direction is related to this uniqueness. Notably, a GGG sequence has recently been used as a spacer to allow mimicking the swing of the lever arm of a myosin motor [55].

It should be pointed out that in the H^+ -PPi synthase, a mechanism of rotation in energy coupling, similar to that of ATP synthase [54], seems impossible since the H^+ translocation and the catalytic site are on the same subunit, as in P-type ATPases. The alternative phosphorylation system, generating PPi, thus would appear to utilize a fundamentally different coupling mechanism from that involved in the ATP synthesis.

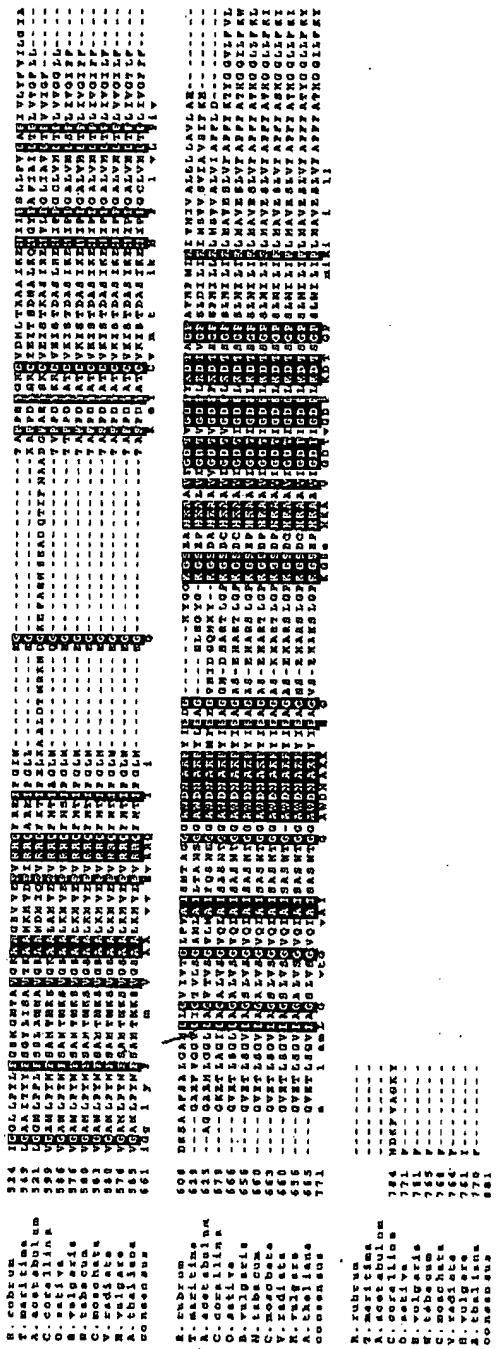
Results from high resolution studies of crystals from soluble PPases [50] indicate that the second motif, DVGADLVGK,

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thetic reactions, thus facilitating the actual biosyntheses. The known PPase families are briefly described in Table 1.

2. The *R. rubrum* H⁺-PPi synthase and homologues from prokaryotes

A very tightly membrane-bound enzyme was found to be responsible for the PPase and the PPi synthase activity [4] in *R. rubrum*. The energetic capacity of PPi was further elucidated when it was possible to drive a reversed electron flow with the energy released by the hydrolysis of PPi [5,6], as well as to create a membrane potential [32-34] over both the chromatophore membrane and artificial membranes. It was also possible in chromatophores to drive the phosphorylation of ADP to ATP in the dark with PPi [8]. The cost of PPi in this experiment was about eight per ATP synthesized, which leads to the question of the proton stoichiometry in PPi hydrolysis. Values obtained vary between 0.5 [10] and two H⁺ [35,36] per PPi hydrolyzed. Very interesting in this connection is that in plasma membrane vesicles from *S. genticanae* [27], the hydrolysis of one ATP yields three PPi and vice versa, three PPi yield one ATP, indicating a H⁺ stoichiometry of one for PPi hydrolysis. The isolated and purified enzyme could be reconstituted in artificial liposomes with a retained activity [37] and when co-incorporated with the complete F₀F₁ complex from *R. rubrum*, ATP synthesis driven by PPi hydrolysis was obtained also in the liposomes [38]. In the bacteria, the PPi synthase is situated in the plasma membrane with the same polarity as the ATP synthase, with the catalytic site towards the cytosol. PPi synthesis and ATP synthesis compete for the available proton gradient, at least in isolated chromatophores [39]. The rate of PPi synthesis, at a saturating light intensity, is 12-15% of the rate of ATP synthesis.

The enzyme is extremely hydrophobic, a property which has caused considerable difficulty in both the original isolation and the determination of the amino acid sequence. Several attempts have been made to make a direct analysis on the isolated and purified protein, all of which have failed, probably due to the high percentage of detergent necessary to keep it active in solution. The cloning and sequencing of the gene encoding the PPase left one problem unsolved. Two possibilities for the start codon of the gene appeared, separated by 126 bp, one yielding a deduced protein of 660 amino acids with a molecular mass of 67453 [22], the other giving a structure with 702 amino acids with the molecular mass 71609 (Fig. 1). The two bacterial H⁺-PPase homologues which both contain more than 700 amino acids are more similar to the longer version of the *R. rubrum* sequence. So is the suggested dimer structure of the *R. rubrum* PPi synthase with a molecular mass of 167.7 ± 30.7 kDa [40], as determined by radiation inactivation. A dimer has also been suggested based on ultrafiltration results [41]. Another argument favoring the 702 amino acid length is that there are only 15 predicted transmembrane segments in the 660 amino acid structure [22], whereas the 702 amino acid one has 16, as have all the other homologues in the H⁺-PPase family. No striking homology with the N-terminals of known H⁺-PPases is

Table 1
Known PPase families

Family	Members
1. Tightly membrane-bound H ⁺ -pumping PPases	a. Bacterial PPases b. Archaeal and bacterial homologues c. Vacuolar PPases
2. Earlier known family of soluble PPases	a. Cytoplasmic PPases (archaeal, bacterial and eukaryotic) b. Mitochondrial (and chloroplast?) PPases (probably soluble parts of H ⁺ pumps)
3. Recently found family of soluble PPases	a. Some archaeal and bacterial PPases

found, but a new homologue from the *Arabidopsis thaliana* genome (Vysotskaja, V.S. et al., GenBank, accession AC005679) shows a particular similarity to the *R. rubrum* sequence, both with respect to the complete protein and to the N-terminal part, unique to its longer version, which is used in this paper. A final conclusion about the actual start may have to await successful sequencing of the N-terminal part of the *R. rubrum* enzyme.

The *Rhodospirillum*, *Pyrococcus* and *Thermotoga* sequences show only about 38-39% identities between themselves, which indicates that they are much more diverged from each other than the higher plant enzymes are. An intriguing question is whether the two prokaryotic H⁺-PPase homologues will be physiologically active and also capable as PPi synthases as those from *R. rubrum* and *R. viridis* [42].

3. H⁺-PPases in plant vacuoles

The main role of V-PPases seems to be to participate in the acidification of vacuoles. In tonoplasts from *Zea mays* L., PPi synthesis has been obtained in response to a H⁺-gradient created by ATP hydrolysis, as well as ATP synthesis in response to a PPi-generated H⁺-gradient [43]. The dependence of V-PPase activity on K⁺ ions [44] has led to a debated suggestion of V-PPase-mediated physiological transport of K⁺ ions into vacuoles [28]. Also, V-PPases probably occur as dimers in vivo [45].

The V-PPase from *Arabidopsis* has been heterologously expressed in yeast [46]. At least four V-PPases have been reconstituted in liposomes [47] with a retained activity. Site-directed mutation studies of *Arabidopsis* V-PPase expressed in yeast have revealed some amino acids of apparent functional importance [48]. E427, located on the cytosolic side immediately after the predicted transmembrane segment 9, is of particular interest since an E427Q mutant preferentially impairs H⁺ translocation over PPi hydrolysis and the E427D mutant enhances H⁺ translocation [48]. E427 is included in a motif, EYY1, present in all sequenced H⁺-PPases, except in *Pyrococcus*, where it is the similar DYYT. D504 is also conserved in the H⁺-PPases and mutant D504N essentially lacks both PPase activity and H⁺ translocation.

The first indicated family relationship between vacuolar and bacterial H⁺-PPases was found when antibodies directed against the V-PPase of *Vigna radiata* cross-reacted with the *R. rubrum* PPi synthase [49]. Both bacterial and vacuolar H⁺-PPases show few sequence similarities with soluble PPases. An

¹ Sequence data were obtained through early release from The Institute for Genomic Research at www.tigr.org and/or through NCBI at www.ncbi.nlm.nih.gov.

To introduce
vacuole in *Arabidopsis*

R. rubrum	GGG I FTK C ADV G ADLVC	- F V E A G I F E D D P R N P A V I A D N V G D N V G D C
T. maritima	GGG V Y T K A D V G A D L V C	- K T E L N I F E D D P R N P A V I A D N V G D N V G D V
P. aerophilum	GGG I Y T K A D V G A D L V C	- F V E A G I F E D D P R N P C V I A D N V C D N V G D V
C. corallina	GGG I X T K A D V G A D L V C	- F V E A G I F E D D P R N P A V I A D N V G D N V G D V
A. acetabulum	GGG I X T K A D V G A D L V C	- F V E A G I F E D D P R N P A V I A D N V G D N V G D V
O. sativa	GGG I X T K A D V G A D L V C	- F V E A G I F E D D P R N P A V I A D N V G D N V G D V
B. vulgaris	GGC I X T K A D V G A D L V C	- F V E A G I F E D D P R N P A V I A D N V G D N V G D V
N. tabacum	GGC I X T K A D V G A D L V C	- F V E A G I F E D D P R N P A V I A D N V G D N V G D V
C. moschata	GGG I Y T K A D V G A D L V C	- F V E A G I F E D D P R N P A V I A D N V G D N V G D V
V. radiata	GGG I Y T K A D V G A D L V C	- F V E A G I F E D D P R N P A V I A D N V G D N V G D V
E. vulgare	GGG I Y T K A D V G A D L V C	- F V E A G I F E D D P R N P A V I A D N V G D N V G D V
A. thaliana	GGG I X T K A D V G A D L V C	- F V E A G I F E D D P R N P A V I A D N V G D N V G D V
consensus	GGG I F T K C A D V G A D L V C	- F V E A G I F E D D P R N P A V I A D N V G D N V G D V
R. rubrum	G G G A W D N A K K Y I E D G - - - H X G G C G S E A H K A A V T G D T V G D P M K D T	
T. maritima	S C G A N D N A K K Y I L D A G N L E - - - G Y - K C S E P H K A D V I G D T V G D P L K D T	
P. aerophilum	A G G A N D N A K K Y I E I Q - - - C L R K T E M H K A D V I G D T V G D P L K D T	
C. corallina	T G C A N D N A K K Y I E S A G G N D H A R T L G P K G S D C H K A D V I G D T V G D P L K D T	
A. acetabulum	S C G A N D N A K K Y I E S G V E I D G - Q M Y Y N G S D A H K A D V I G D T V G D P M K D T	
O. sativa	T C G A N D N A K K Y I E A G A S E H A R T L G P K G S D C H K A D V I G D T V G D P L K D T	
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N. tabacum	T G A W D N A K K Y I E A G A S E H A R T L G P K G S D C H K A D V I G D T V G D P L K D T	
C. moschata	T G C A W D N A K K Y I E A G A S E H A R T L G P K G S D C H K A D V I G D T V G D P L K D T	
V. radiata	M T C A W D N A K K Y I E A G A S E H A R T L G P K G S D C H K A D V I G D T V G D P L K D T	
E. vulgare	T G C A W D N A K K Y I E A G N S E H A R T L G P K G S D C H K A D V I G D T V G D P L K D T	
A. thaliana	T G C A W D N A K K Y I E A G V S E H A R T L G P K G S D C H K A D V I G D T V G D P L K D T	
consensus	G A W D N A K K Y I E A G V S E H A R T L G P K G S D C H K A D V I G D T V G D P L K D T	

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4.1. Within the H⁺-PPase family

Attention is here first restricted to corresponding parts of two loops in the PPi synthase from *R. rubrum*. A 45 amino acid piece from the 57 amino acids in the putative active site loop 5 is compared with a similar part of loop 15, which may contain a duplicated and subsequently evolved segment of an ancestral version of loop 5. Three motifs of loop 5 are GGG, DVGADLVGK and DNVGDNVGD.

The first motif, the triglycyl sequence, occurs in all H⁺-PPase family members and may be expected to have the potential to provide, to the extent that other structural properties of the enzyme allow, an unusually high local conformational change capability. In the PPi synthase, uniquely, the loop 15, with the 'duplicated segment', contains a similarly positioned sequence of three glycyl residues, in contrast to just two or one in all other known H⁺-PPases (Fig. 3). In view of the conformational change mechanism of the ATP synthase function [53,54], one may ask the question if the fact that only the PPi synthase of the H⁺-PPase family may function physiologically in the PPi synthesis direction is related to this uniqueness. Notably, a GGG sequence has recently been used as a spacer to allow mimicking the swing of the lever arm of a myosin motor [55].

It should be pointed out that in the H⁺-PPi synthase, a mechanism of rotation in energy coupling, similar to that of ATP synthase [54], seems impossible since the H⁺ translocation and the catalytic site are on the same subunit, as in P-type ATPases. The alternative phosphorylation system, generating PPi, thus would appear to utilize a fundamentally different coupling mechanism from that involved in the ATP synthesis.

Results from high resolution studies of crystals from soluble PPases [50] indicate that the second motif, DVGADLVGK,

EXHIBIT C



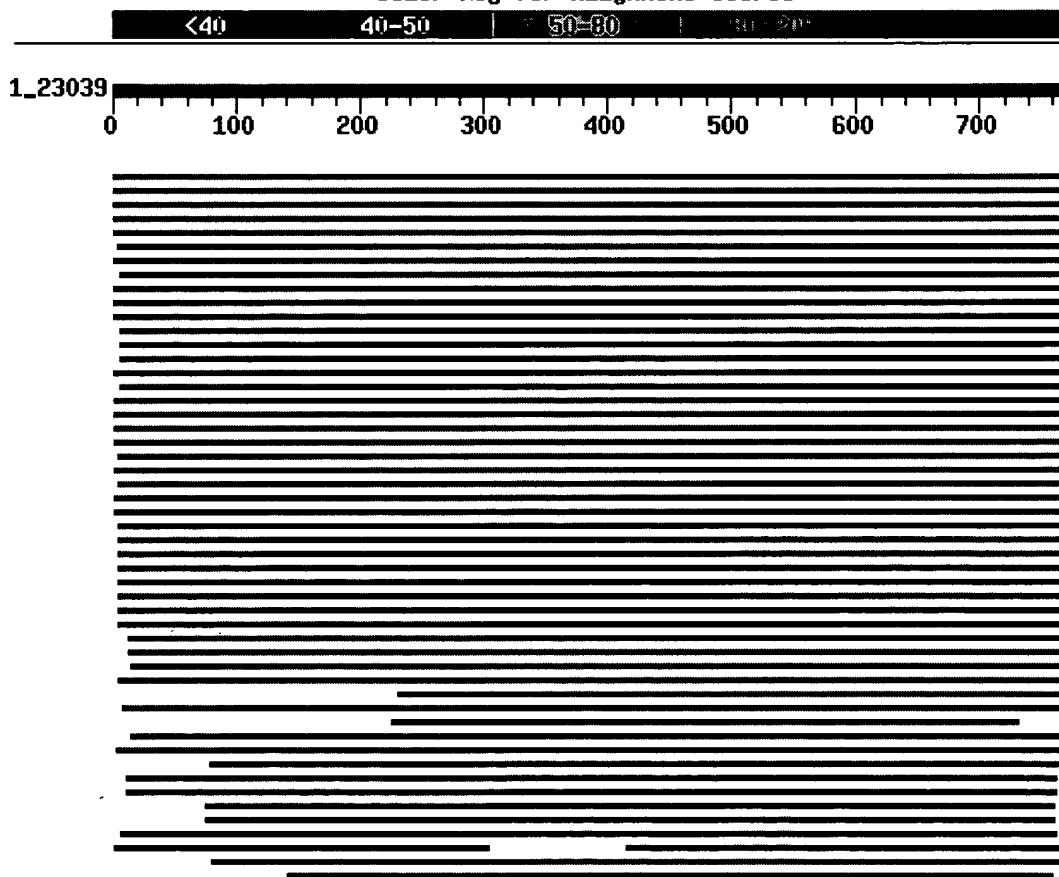
BEASTP 2.2.9 [May-01-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.

Distribution of 100 Blast Hits on the Query Sequence

Color Key for Alignment Scores



Plants (mono and dicots)	% Identity at the amino acid level
<i>Lycopersicon esculentum</i> (Tomato)	89
barley	81
<i>Oryza sativa</i> (rice)	82
<i>Nicotiana tabacum</i> (common tobacco)	84
<i>Prunus persica</i> (peach)	84
<i>Cucurbita moschata</i> (butter-nut squash)	83
<i>Beta vulgaris</i> (sugar beet)	84
<i>Triticum aestivum</i> (wheat)	80
<i>Vitis vinifera</i> (grapes)	78
<i>Hordeum brevisubulatum</i> (wild barley)	82
<i>Pyrus communis</i> (common pear)	84
<i>Chenopodium rubrum</i> (red goosefoot)	83
<i>Hevea brasiliensis</i> (rubber tree)	84
<i>Vigna radiata</i> (mung bean)	82
<i>Thellungiella salsuginea</i> (Salt-lick mustard)	90
<i>Chara corallina</i> (green algae)	67
<i>Chlamydomonas</i> <i>reinhardtii</i> (algae)	61
Parasites	
<i>Trypanosoma brucei</i> (parasite)	51
<i>Leptospira interrogans</i> (spirochete)	54
<i>Toxoplasma gondii</i> (parasite)	48
<i>Plasmodium falciparum</i> (parasite)	49

